GeneChip[™] Command Console[™] (GCC) v7.0 USER GUIDE

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13	August 2019	Software release v6.1. Wash only option added to the Multi-Channel (MC) Instrument. Enhanced log file collection functionality.
12	March 2019	Software release v6.0. Scan only option using the GCC GeneTitan Scanner. Wash only option added to the GeneTitan System. Updated branding.
11	January 2019	Software release v5.0. Windows 10 Enterprise 2016 LTSB only. Features Thermo Fisher Cloud connectivity for monitoring instruments remotely.
10	June 2013	Documented new features for v4.0 release. Version 4.0 supports the new 384 plate format (GeneTitan Multi- Channel Instrument Control ONLY) and is now compatible with Windows 7 Professional with SP1.Minio
9	February 2013	Minor v3.2 revisions to documentation.
8	June 2011	Documented new features for v3.2 release. The Viewer now monitors the progress of array data through the workflow and updates to the GeneTitan Instrument Control software to improve reliability.
7	July 2010	Software release v3.1.1.
6	April 2010	Software release v3.1.
5	November 2009	Documented new features for v3.0 release. Version 3.0 supports the new genotyping array plate used with GeneTitan Multi-Channel (MC) Instrument. Version 3.0 also allows you to control the GeneTitan family of instruments to process array plates from hybridization to scanning.
4	November 2008	Minor 2.0 revisions to documentation.
3	October 2008	Documented new features for v2.0 release. Register plate, array, and sample data for Array Plates and control the GeneTitan Instrument to process array plates from hybridization to scanning with no user intervention.
2	March 2008	Software release v1.1.
1	August 2007	Initial release.

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Introduction



The development of microarray technology means that researchers can now perform more experiments and collect more data from each experiment than ever before. Researchers need to analyze and organize this mass of data, which presents new challenges for the researchers and the software they use.

GCC provides flexible and powerful tools for:

- Entering and organizing information about the sample and GeneChip probe arrays.
- Controlling the instruments used to process probe arrays and collect the intensity data.
- Tracking the progress of an array through the array processing workflow.
- Working seamlessly with other tools for downstream analysis.

There are several GCC configurations:

- GCC and GeneChip Scanner 3000 system (GCS3000 and FS450)
- GCC and GeneTitan[™] system
- GeneTitan Multi-Channel (MC) Instrument
- GCC Only
- GCC and GeneTitan Scanner system
 - GeneTitan Scanner Instrument

New features in v7.0

• The About Box now displays the detected camera.

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Getting started



GCC provides tools that enable you to process arrays, extract the intensity data for use by the probe level analysis software, and organize the resulting sets of data files.

You can use GCC to process:

- Cartridge Arrays
- Array plates for the GeneTitan MC instrument

See "Different array types" on page 16 for more information about the differences in the arrays.

IMPORTANT! Before running GCC for a particular GeneChip Array, you must have the library files for that array type installed on your computer.

To fully use the capabilities of GCC, you need to understand:

- The components of the software
- The array processing workflow that the GCC components perform
- · The types of files that GCC produces and uses
- The structures and tools that GCC uses to organize the resulting data

This chapter describes the above concepts in:

- "GCC components" on page 18
- "Array processing workflow" on page 23
- "File types in GCC" on page 28
- "Organizing data" on page 32

Different array types

The GCC software may be used to process both cartridge arrays and array plates for the GeneTitan MC instrument.



An array cartridge contains a single array, which is processed on its own through washing and staining and scanning by using the GCC Fluidics Control and GCC Scan Control with the FS-450 Fluidics Station and the GCS3000 scanner. Hybridization is performed using instruments that are not controlled by the GCC software. The array cartridge is identified by a bar code that can be scanned and used to track the array workflow.

Multiple arrays can be scanned sequentially if you use the GCS 3000 AutoLoader.

A 384 or Mini-96 format array plate can be used on the GeneTitan MC instrument. A 96-format array plate may contain 16, 24, or 96 arrays.

All the arrays on the plate are processed from hybridization to scanning using the GeneTitan MC instrument and the GCC GeneTitan Control software. This enables increased automation and consistency in processing when dealing with large numbers of samples



The array plate has a barcode for tracking. Each individual array on the plate is identified by its row and column. For example, the circled array in the figure below is array D05.

GCC components

The features and functions of GCC vary depending upon which instrument or instruments it is being used with.

GCC is comprised of the following components:

- GCC Portal: software for sample registration, data organization, and tracking the array processing workflow. GCC Portal uses a web interface for user access.
- Other GCC components are installed on your computer and run behind the scenes on your computer. These include the Indexer, a service that tracks the relationships of files in the GCC data roots. The information is used to keep track of the GCC files, for example, in the Folders and Projects views. The services typically run behind the scenes without user control, but you may need to change their configuration in some circumstances. See "GCC services" on page 35 for more information.
- GCC Fluidics Control and GCC Scan Control for processing cartridge arrays:
 - GCC Fluidics Control: Software for running the Fluidics Station 450.
 - GCC Scan Control: Software for the GeneChip Scanner 3000 (GCS 3000) and GCS 3000 with AutoLoader (AutoLoader).
- GCC GeneTitan Control and GCC GeneTitan Scanner for processing array plates:
 - GCC GeneTitan Control software for running the GeneTitan Multi-Channel (MC) instrument.
 - GCC GeneTitan Scanner for running the GeneTitan Scanner instrument.

IMPORTANT! A system used as a GeneTitan workstation requires a user account with specific privilege settings. In addition, some of the other features of Windows 10 Enterprise 2016 LTSB must be set up in particular ways or disabled to avoid causing problems when running GeneTitan IC software.

Your system has been set up for use with GeneTitan with the user account AFFXUser. This account has these privileges and features already set up.

• GCC Viewer: Software for viewing image data and workflow status and performing manual gridding.

These tools are used to install necessary files or manage other GCC functions:

- Library File Importer
- Fluidics Script Importer
- GeneTitan Library File Installer
- Data Upload Scheduler
- Email Configuration Editor

Before using GCC

Required Operating System	GCS3000/FS450	GeneTitan MC	GeneTitan	Analysis Only
	Instrument	Instrument	Scanner	Workstation
Windows [®] 10 Enterprise 2016 LTSB	Yes	Yes	Yes	Yes

The following prerequisites must be met:

- The necessary GCC components are installed.
- The proper Data Root is set up and selected.
- See "Adding a data root" on page 76.
- Libraries are installed for the probe array types you want to process.
- The correct fluidics scripts are installed for the probe array types you want to process.
- See "Installing protocols" on page 172.
- If using remote network data storage or linked instrument control systems, you need to perform additional configuration.

See Appendix A, "Networking" on page 338.

Note: GeneChip Command Console (GCC) software has been validated for use with your Operating System's built-in Windows Defender anti-virus software. Using other anti-virus software is not recommended, as it may cause incompatibility issues.

Starting the GCC launcher

IMPORTANT! GCC Launcher menu options vary, as they are based on the type of GCC software that was installed.

> 1. Click Start \rightarrow Thermo Fisher Scientific \rightarrow GCC Launcher or double-click on the GCC Launcher shortcut on the desktop.

The appropriate Launcher appears:

- "GeneTitan MC" on page 20
- "GCS3000 with fluidics" on page 21
- "Analysis only" on page 22

GeneTitan MC

GCC Launcher — × Command Console	Figure 3 GCC Launcher menu - GeneTitan MC	
Command Console Image: GCC Software Portal Image: GCC Data Uploader Resources Image: Support at thermofisher.com Image: NetAffx	🖉 GCC Launcher — 🗆 🗙	
	Command Console Image: GCC Software Portal Image: GCC Software Portal Image: Command Console Viewer Image: Gene Titan Instrument Control Tools Image: Gene Titan Instrument Control Tools Image: Gene Titan Library File Installer Image: Gene Titan Library File Installer	

Command Console

- GCC Software Portal (See "GCC portal home page" on page 48)
- Command Console Viewer (See Chapter 9, "Using the GCC viewer" on page 267)
- Gene Titan Instrument Control (See Chapter 8, "Controlling the instruments" on page 223)

Tools

- Thermo Fisher Cloud Administration (See "Monitoring an instrument remotely" on page 36)
- GeneTitan Library File Installer (See Appendix D, "Installing library files and scripts" on page 360)
- Email Configuration Editor (See Appendix E, "Notification e-mails" on page 367)
- GCC Data Uploader (See "Scheduling auto-uploads" on page 96)

Resources

- thermofisher.com (Home page)
- Support at thermofisher.com (Services and support page)
- NetAffx (Home page)

GCS3000 with fluidics



Command Console

- GCC Software Portal (See "GCC portal home page" on page 48)
- Fluidics Control (See Chapter 6, "Controlling the fluidics station" on page 150.
- **Scan control** (See Chapter 7, "Scanning cartridge arrays" on page 179)
- Viewer (For more information, see Chapter 9, "Using the GCC viewer" on page 267)

Tools

- Library File Importer (See Appendix D, "Installing library files and scripts" on page 360)
- Fluidics Script Installer (See "Installing protocols" on page 172)
- Log Collector (See "Collecting GCS3000/FS450 log files" on page 371)
- Reconnector (See Appendix H, "Reconnector" on page 375)
- GeneTitan Library File Installer (See Appendix D, "Installing library files and scripts" on page 360.)

- Email Configuration Editor (See Appendix E, "Notification e-mails" on page 367.)
- Data Uploader (See "Scheduling auto-uploads" on page 96)

Resources

- thermofisher.com (home page)
- Support at thermofisher.com (services and support page)
- NetAffx (home page)

Analysis only

Figure 5 GCC Launcher menu - Analysis only
🖉 GCC Launcher – 🗆 🗙
Command Console GCC Software Portal Command Console Viewer Tools
Gene Titan Library File Installer
CCC Data Uploader Resources themofisher.com Support at themofisher.com
Net Affx

Command Console

- GCC Software Portal (See "GCC portal home page" on page 48)
- **Command Console Viewer** (For more information, see Chapter 9, "Using the GCC viewer" on page 267)

Tools

- Library File Importer (See Appendix D, "Installing library files and scripts" on page 360)
- Reconnector (See Appendix H, "Reconnector" on page 375)
- GeneTitan Library File Installer (See Appendix D, "Installing library files and scripts" on page 360.)
- Data Uploader (See "Scheduling auto-uploads" on page 96)

Resources

- thermofisher.com (home page)
- Support at thermofisher.com (services and support page)
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Array processing workflow

GCC is used to process the arrays used in your experiment. While GCC provides several options and alternatives for processing arrays, the recommended workflows for cartridge arrays (Figure 6) and for array plates (Figure 7) enable you to include data about the sample and experiment and to easily track the processing steps for the cartridge array or array plate.



In the recommended array processing workflow for cartridge arrays, you create a sample file as the first step, assigning sample attributes and a physical array or arrays to the sample. You then:

- Hybridize the array and sample (step not controlled using GCC)
- Wash and stain the array(s)
- Scan the array(s) to create Image data (DAT) files.

After that, GCC aligns a grid on the DAT files and computes the Cell Intensity data (CEL) file.



In the recommended array processing workflow for Array Plates, you create sample files for all the arrays on the array plate as the first step. The Hybridization, Fluidics, and Imaging of the array plates are completed using the GeneTitan MC instrument. After that, GCC aligns a grid on the DAT files and computes the Cell Intensity data (CEL) file.

The CEL data generated in the GCC software from array plate data or cartridge data can be used by other software packages for data analysis.

The workflow steps are described in more detail in the following sections:

- "Registering samples and arrays" on page 25
- "Hybridizing arrays and samples" on page 26
- "Washing and staining the arrays" on page 26
- "Running scanners" on page 27
- "Tracking gridding and CEL file generation" on page 27

The GCC Sample and data files that are created during the workflow are described in more detail in "File types in GCC" on page 28.



Registering samples and arrays

In GCC, the Sample file is the beginning of the data chain for a given experiment. The sample information is stored in a Sample file with an ARR extension. The arrays used in analysis and data files produced by analysis are linked to this Sample File.

The information about the sample(s) and experiment(s) are collected as attributes. These attributes can then be used to locate particular Sample files in filtering and search operations.

The links between the sample and data files and the GCC tools used to generate the sample files are described in more detail below:

- "Template and user attributes" on page 25
- "Sample registration options" on page 25

Template and user attributes

There are two types of sample attributes in GCC:

- Template Attributes
- User Attributes

Template attributes

A template in GCC is a list of attributes that can be assigned to a Sample file. When you create a template, you can specify:

- The attributes included in the template.
- The data type for each attribute.
- Whether the attribute is required.
- Value options for a controlled data attribute.

After you have created a template you can assign the template to a new Sample file during Batch Registration (for cartridge arrays). This automatically adds all the attributes in the template to the Sample file. You can then enter values for each attribute. This enables you to standardize the attributes that are assigned to samples.

The template functions are described in "Working with templates" on page 328.

User attributes

User attributes are created dynamically during the registration of a sample and array. This enables you to create a quick note for a particular sample file.

User attributes are not listed in a template; they have usually been added to a specific sample file. They can be used in filtering and search operations, just like the template attributes.

Sample registration options

GCC provides multiple ways to create Sample files. To select the best one for your operation, evaluate:

- Whether you are creating sample files for cartridge arrays or array plates.
- The number of arrays you are going to be processing.
- Whether you want to enter sample attributes during registration.
- Whether you want to enter attributes at a later time.
- Whether you are creating sample files for samples that were processed in a 96well sample prep plate.

For example:

- Batch Registration enables you to create a group of Sample files for cartridge arrays; you can assign attributes to each Sample file, along with one or more arrays.
- Detailed Registration creates a single Sample file for a cartridge array; you can assign attributes and one or more arrays to the sample file.
- Quick Registration creates multiple sample files for cartridge arrays, each with a single array and no attributes (attributes can be entered later).
- Sample Prep Plate Registration creates sample files for cartridge arrays for samples in up to two 96-well plates.
- Array Plate Registration creates the sample files for the arrays on an Array Plate for the GeneTitan MC System.
- Editing functions correct problems or add attributes to previously created sample files.

The Sample registration options are described in Chapter 5, "Creating and editing sample (ARR) files" on page 101.

In addition, the Drop and Scan feature enables you to create a sample file for an array when the array is scanned. Drop and Scan is available for:

- Cartridge arrays (see "Drop and scan" on page 206)
- Array Plates (see "Drop and scan with array plates" on page 260)

Hybridizing arrays and samples

For GeneChip cartridge arrays, hybridization is not controlled using the GCC software.

For Array Plates, the hybridization is controlled using the GCC GeneTitan MC Control software (see Chapter 8, "Controlling the instruments" on page 223).

Washing and staining the arrays

Different instrumentation and instrument control software used to process Cartridge Arrays and Array Plates.

Cartridge arrays

The Fluidics Station 450 (FS450) is used to hybridize, wash, and stain the GeneChip arrays (called arrays in this manual). The FS450 can independently process an array using a different fluidics protocol in each of four different modules.

The GCC Fluidics Control software is used to control the FS450. A workstation with GCC Fluidics Control software and a Sealevel card installed can control up to eight different fluidics stations. The software and its uses are described in Chapter 6, "Controlling the fluidics station" on page 150.

Array plates

The arrays on the Array Plate are washed and stained using the GeneTitan MC instrument, controlled using the GCC GeneTitan Control software. The software and its use are described in Chapter 8, "Controlling the instruments" on page 223.

Running scanners Different IC software and instrumentation are used to scan:

- Cartridge Arrays
- Expression Array Plates
- Genotyping Array Plates

Cartridge arrays

The array is scanned after hybridization, washing, and staining, using one of the following scanners:

- GeneChip Scanner 3000 (GCS3000) (scans one chip only)
- GCS3000 with Autoloader (load up to 48 chips for scanning without operator attention)

The GCC Scan Control Software is used to control the scanner. The software and its use are described in Chapter 7, "Scanning cartridge arrays" on page 179.

Expression array plates

The arrays on the array plate are scanned using the GeneTitan MC instrument, controlled by the GCC GeneTitan Control software.

The software and its uses are described in Chapter 8, "Controlling the instruments" on page 223.

There are some differences in how the arrays from array plates are scanned and the data is managed, as described on "GeneTitan array plates" on page 271).

Genotyping array plates

The arrays on the genotyping array plates are scanned using the GeneTitan MC Instrument, controlled by the GCC GeneTitan Control software.

The software and its uses are described in Chapter 8, "Controlling the instruments" on page 223.

There are some differences in how the arrays from array plates are scanned and the data is managed, as described on "GeneTitan array plates" on page 271).

Tracking gridding and CEL file generation

- After the array has been scanned, GCC:
 - Aligns a grid on the Image (DAT) file to identify the probe cells.
 - Computes the probe cell intensity data for the array and creates a CEL file.
 - Generates JPG and RPT files.

The GCC Viewer enables you to track the progress of this step in the workflow and manually correct gridding problems, if necessary. The Viewer and its uses are described in Chapter 9, "Using the GCC viewer" on page 267.

File types in GCC

Different types of information are collected by GCC in different types of files:

- Information about the sample and experiment are collected in Sample files (see "Sample files", below)
- Probe array data generated during scanning and processing are collected in Data files of various types (see "Tracking files with GUIDs" on page 29).
- Audit and Log files contain information about array processing and other processes (see "Other file types" on page 31)

Globally Unique Identifiers (GUIDs) are used to track the relationships between Sample files, physical arrays, and Data Files (see "Tracking files with GUIDs" on page 29)

Sample files The Sample (ARR) file (Figure 8) collects two types of information:

• Sample Attributes: information that you can use to interpret the experimental data. It can include information about the sample itself, the experimental conditions, or other information you may find useful.

You can use the attributes to search for particular files; some attributes can be used by the probe level analysis software during analysis. You can use templates to manage the attributes used for a particular experiment (see "Template and user attributes" on page 25 for more information).

• Array Information: Information about the array(s) used with the sample. More than one array can be associated with the sample. This is useful for tracking replicates; in addition, it can be used to simplify tracking data for multi-chip arrays.

Each array is assigned an array name during registration. The array name is used to identify the DAT, CEL, and CHP data files that are generated during analysis.



Tracking files with GUIDs

A GUID, or Globally Unique Identifier, is assigned to each file for tracking (Figure 9). GUIDs are numbers generated to track a file that are unique to that file.

Figure 9 GUIDs in Sample and Data Files				
📔 Sample (ARR) File	Image (DAT) File(s)	Intensity (CEL) File(s)	Probe Intensity (CHP) File(s)	
File Name: Sample1.ARR Sample1 ARR File GUID	File Name: Sample1Array1.DAT	File Name: Sample1Array1.CEL Sample1Array1 CEL File GUID	File Name: Sample1Array1.CHP Sample1Array1 CHP File GUID → Sample1Array1 CEL File GUID	
Array Name: Sample1Array1 Sample1Array1 Array GUID —	Sample1Array1 DAT File GUID → Sample1Array1 Array GUID →	→ Sample1Array1 DAT File GUID → Sample1Array1 Array GUID	→Sample1Array1 DAT File GUID →Sample1Array1 Array GUID	
Array Name: Sample1Array2 Sample1Array2 Array GUID —	File Name: Sample1Array2.DAT Sample1Array2 DAT File GUID Sample1Array2 Array GUID	File Name: Sample1Array2.CEL Sample1Array2 CEL File GUID Sample1Array2 DAT File GUID	File Name: Sample1Array2.CHP Sample1Array2 CHP File GUID Sample1Array2 CEL File GUID Sample1Array2 DAT File GUID Sample1Array2 Array GUID	

During Sample registration the Sample file is assigned a Sample File GUID. In addition, an Array GUID is provided for every array name entered.

Every data file (DAT, CEL, and CHP) generated for an array will contain the Array GUID for the array, as well as the GUIDs for each of its parent data files.

The GUIDs enable you to trace the lineage of any data file independent of the file name.

Data files

A set of data files is produced for each array in the Sample file. (Figure 9)

The data files include:

- "Image (DAT) file"
- "Intensity (CEL) data files" on page 30
- "Probe analysis (CHP) Files" on page 30

Each file is assigned a GUID, or Globally Unique Identifier, to be used in tracking the relationships between Sample files, physical arrays, and data files. See "Tracking files with GUIDs" on page 29 for more information.

Image (DAT) file

The DAT file contains pixel intensity values collected from the scanner, along with the gridding information used during feature extraction.

When a DAT file is regridded, the underlying data used by previously generated CEL files is changed. A new GUID is assigned to the regridded DAT file, breaking the link to any previously generated CEL files. The CEL files are linked with the array via array GUIDs, but not to the regridded DAT file. CEL files generated after regridding are linked to the new DAT file via the DAT file GUID and to the array by the array GUID.

Intensity (CEL) data files

The CEL file stores the results of the intensity calculations on the pixel values of the DAT file. This includes an intensity value, standard deviation of the intensity, the number of pixels used to calculate the intensity value, a flag to indicate an outlier as calculated by the algorithm and a user defined flag indicating the feature should be excluded from future analysis. This data is used by the CHP writer software to extract the actual data of interest.

JPG files

JPEG files are a copy of the DAT file in a standard image file format; they provide an image file with a reduced file size for QC inspection, archiving, and publication.

Probe analysis (CHP) Files

These files, which have file extensions ending in CHP, contain the probe analysis data for the array. They are produced by the Analysis Application software and contain the actual data of interest (SNP calls, expression data, etc., depending upon the array type).

Other file types Audit and Log files track the tasks performed by different software components.

Audit files

An Audit file is an XML file that tracks the processing of each physical array processed by GCC. An Audit file is produced for each physical array and tracks all the processing steps that were performed on the array, including multiple scannings and regridding.

The audit file has the same root name as the physical array.

See "Viewing audit files" on page 65.

Log files

Log files are produced by different GCC components. The logs provide a record of the tasks performed by different components, such as the migration tools and the installer.

These log files may provide useful information for troubleshooting problems.

See Appendix F, "Log files generated by GCC" on page 369 for more information.

2

Organizing data

To use GCC, you need to understand the structures and tools the software provides for organizing your data during and after generation.

This section describes:

- "Folders" on page 32
- "Projects" on page 34
- "Data organization tools in GCC" on page 35
- "GCC network functionality" on page 35

Folders

GCC uses the Windows file folders on your hard drive to organize your data.

Note: A folder must be designated as an GCC data root, or must be a sub-folder of a designated GCC data root, for the files in that folder to be tracked by GCC (Figure 10).

Figure 10	Organization of files in GCC
	Windows [®] File Folder (not associated with GCC)
	C:\Command_Console\Data Root 1 (on user's computer)
	Sample File X
	Subfolder 1 [Project A]
	Sample File A1
	Sample File A2
	SubFolder 2 (not associated with project)
	Sample File F1
	C:\Command_Console\Data Root 2 (on user's computer)
	Subfolder 1 [Project C]
	Sample File C1
	Isharename'share'Wetwork Data Root (on network storage)
	Subfolder 1 [Project D]
	Sample File D1

Windows file folders

These are folders that are on your hard drive, but have not been assigned to a GCC Data Root, either directly or by a parent/child relationship.

These file folders are not searched by the Indexer and the files in them are not displayed in the GCC Portal. You can copy GCC files to a system folder using different GCC Portal functions, which is useful for sharing data with other users.

Data roots and sub-folders

A Data Root is a folder that has been specified for Command Console data. Data roots are searched by the Indexer and the files in them are listed in the GCC Portal.

Note: On instrument control workstations, the default data root has to be on the local drive and cannot be a USB or an external network drive.

A default data root is created when the software is installed. You can assign other folders as data roots, too. A data root can be on the computer running GCC, or on a network data storage computer connected with a Windows network.

A data root on a local drive is indicated as a local drive path: C:\Command Console\Data for example.

Data roots on networked computers are specified using Universal Naming Convention (UNC) paths as $\server\share\filepath$.

A sub-folder is a child folder created within a data root. The sub-folder and its files are also searched by the indexer and listed in the GCC Portal.

For information about setting the data root, see "Managing data roots" on page 75.

For information about using a data root on a different computer on a Windows network, see Appendix A, "Networking" on page 338.

The data roots and sub-folders and their contents are displayed in the Folder view (see "Folder view" on page 50).

File and folder security

You can use the Windows Sharing and Security settings to control access to your data when using network functionality. GCC supports setting permissions at the folder level, not the file level, even though the Windows settings can be set at the file level. You can change the settings for Sharing, permissions, and security for a selected file, but you need to be very careful about setting permissions when using GCC; you could lock yourself out of your own data or deny access to other people if the permissions are set incorrectly. **Work with your IT department for help in setting the permissions**.

For more information, see Appendix B, "Windows sharing and security issues" on page 348.

Default folders

A Default folder is a data root or sub-folder that has been set as a destination folder for files produced when certain operations are performed:

- Sample and data files produced when performing Drop and Scan.
- Data files for an array that is registered to a Sample file located on network data storage.

For more information, see:

- "Specifying a default folder" on page 90
- "Drop and scan" on page 206
- "Drop and scan with array plates" on page 260
- "GCC network functionality" on page 35
- "The Status window (Figure 211) displays the following information:" on page 182

Projects

A project is a label assigned to a Data Root or sub-folder; the project label can be used to organize Sample and data files. If you assign a project name to a Data Root or sub-folder, all the Sample and data files in that folder are assigned that project name. Any child sub-folders of that project folder are assigned the project name, as well.



Projects have the following characteristics:

- Any Data Root or sub-folder can be a project.
- All sub-folders in a project folder are automatically a part of that project.
- One folder can be a member of more than one project.
- Folders in different locations can be in the same project.

After assigning a project name to a data root or sub-folder, any Sample file placed in that data root or sub-folder is assigned to the project. You can then use the project label to:

- Display file lists grouped by project
- · Search on data limited to a project
- Create a spreadsheet listing the Sample (ARR) files assigned to the project with their attributes. The list can be reviewed as a summary of the project information or used to edit the Sample (ARR) file content using Batch Edit.

You can also assign a sample file to a project during its creation. This places the Sample File and the associated data files in the folder assigned to the project name.

You can move files between projects using Windows Explorer.

For more information, see "Using projects to organize data" on page 78.

Data organization tools in GCC

The data organization tools in GCC enable you to:

- View the files in data roots and folders
- Create and manage projects
- Search for files of interest by various attributes, including sample attributes entered during registration.
- Add and remove Data Roots
- Upload data to a data root

Note: To perform data management functions, you must use Windows Explorer.

See Chapter 4, "Portal and data organization" on page 47 for more information on the data organization tools.

GCC services

The following GCC Services run (in the background) on your computer:

The following GCC Services run (in the background) on your computer:

- GCCAuditLogger
- GCCIndexer.
- GCCTaskManager
- GCCWebServer
- GCC WorkflowBroadcastService: This service enables the instrument to notify analysis applications that data is available for analysis.
- **GCC DeepLaserService**: This service enables the instrument to send notifications and upload data to the Thermo Fisher Scientific Cloud.

Note: If using network functionality, you may need to change the configuration of these services. See "Configuring GCC services" on page 344.

Displaying GCC WebServer status

For GCC, the GCC WebServer enables the display of the GCC Portal pages; it must be running to use GCC Portal. By default, it starts when the computer boots up.

Normal operation is indicated by an icon in the right side of the Taskbar (Figure 12).



GCC network functionality

When GCC is installed on a system, then connected to a Windows network, it provides additional functionality with options for running the array processing workflow and organizing data. These functions include:

- Consolidating the data from multiple GCC workstations on network data storage.
- Performing different parts of the workflow for an array on different workstations while consolidating the data on a single workstation.

You may need to change the settings for some GCC Services to use the network functionality. See Appendix A, "Networking" on page 338 for more information.



Monitoring an instrument remotely

Creating a cloud account

Before you can access and monitor an instrument remotely, you must first create a Thermo Fisher Cloud account.

Note: The Cloud account option is ONLY available on the GeneTtian GCC Launcher.

 Double-click on the GCC Launcher Desktop shortcut The Launcher window appears.



2. Double-click Thermo Fisher Cloud Administration.

The Cloud Administration window appears. (Figure 13)

IMPORTANT! Before signing up: a) You must have an active Internet connection. b) The **Enable Thermo Fisher Cloud Connectivity** check box must be checked, as shown in Figure 13.

Figure 13 Thermo Fisher Cloud	Administration	
applied biosystems	Thermo Fisher Cloud Administration –	□ ×
☑ Enable Thermo Fisher Cloud Conne	ectivity	
Add User		
If you do not have a Thermo Fisher Scientific a	account or forgot your password: CLICK HERE	
Connected Users		
User Name		
Delete User		
Generate Log Files Number of Days		
Select Days	✓ Upload Logs	
3. Click CLICK HERE, as shown in Figure 13.

The Thermo Fisher Connect web page appears.

- 4. Click **SIGN UP NOW**.
- A registration page appears.
- 5. Complete all fields, then click **Create account**.

After a few moments, you will receive an email confirming you have been successfully added to the Thermo Fisher Cloud.

Adding users

IMPORTANT! You cannot add a user(s) while the instrument/scanner is running.

1. Click Add User.

The Add user window appears with an auto-generated QR code graphic and code, as shown in Figure 14.

Figure	14 Add user					
a pplied biosy	tems	Thermo Fisher Cloud Administration 🗕 🗖	×			
<mark>⊡</mark> Enabl	Enable Thermo Fisher Cloud Connectivity					
0 alab						
If Scan th Non-sr 1. 2. 3. 4.	ne auto-generated QR code grap nart phone users: Go to: apps.thermofisher.com/ Click on the Add an Instrumen From the Add an instrument d Enter the generated QR code,	> nic using the "Instrument Connect" Mobile App from Thermo Fisher Scientific. apps/ic/#/ t button. rop-down menu, select GeneTitan, then click Next. then click Send.	×			
		V1B3ZX	-			
		Ok				



Connecting to an instrument remotely

Smart phone (Android OS 5.0+ and iOS 9.0+ only)

users

- 1. Go to your smart phone's application store and download Instrument Connect.
- 2. Install the app as you normally would, then follow the registration and/or sign in instructions.
- 3. Use the Instrument Connect app to scan the auto-generated QR code graphic.
- Non-smart phone 1. Go to: apps.thermofisher.com/apps/ic/#/ The Instrument Connect page appears.
 - 2. Click the Add an Instrument button (upper right). The Add an instrument window appears.
 - 3. Click the drop-down menu, select GeneTitan, then click Next. After a few moments, you will receive an email confirming your instrument has been successfully added to your Thermo Fisher Cloud account.
 - 4. Open the email and confirm its content coincides with the specific instrument you wanted to connect to, then click on the Thermo Fisher Instrument Connect hyper-link.

Your browser opens to a Thermo Fisher Scientific/Returning Customer web page.

- 5. Enter your User Name and Password, then click Sign In. A Thermo Fisher Cloud Terms of Use window appears.
- 6. Review and acknowledge the terms, then click Accept.

The Instrument Connect web page appears (Figure 15) and you are now remotely connected to the instrument.

Figure 15 Instrument Connect web page									
=	InstrumentConnect		Pov	vered by Thermo	o Fisher Cloud				
* 6 11	Connect your instruments, select your 3 favorites and monitor	r them Manager		0	Manage users	More info	🝵 Disconnect	★ Make favorite	
• ••	OD100120-E0100370 GeneTitan_Alex_VM RUNNING	Hybridization Running Next plates ca	Fluidics Idle n be added at 3/27/2	Imager Idle 018 1:01 PM					

The Instrument Connect page features the Instrument's custom tile (Figure 15) that displays the current operational status of the instrument.

- Idle Instrument is on standby and ready for use
- Running Instrument is in use.
- Unknown Instrument has stood idle for more than 24 hours.

3



Managing users (optional)

If you are the Administrator or the first to log into the instrument, the **Manage users** link (Figure 15) is enabled (shown in blue).

1. Click on Manage users.

The Manage users window appears. (Figure 16)

Disconnect
)

- To add a user, return to the Thermo Fisher Cloud Administration window. (Figure 13 on page 36)
- To remove a user, click to highlight the user you want to remove, then click on the trash can icon.
- Click **Close** to close the window.

3

Viewing the instrument status in detail

- 1. Double-click on the Instrument's custom tile.
 - The details page appears. (Figure 17)

Figure 17 In	strument Connect	web page		
≡ GeneTitan MC		Powered by Thermo Fis	her Cloud 🔕	📭 🚱 US 📥 🗸
	Flybridization	Fluidics	Imager	₽ Lamp
	Position 1 Idle Position 2 Idle	550094111111111111111 Will finish at 3/27/2018 1:00 PM	Idle	Remaining lamp 397 hours
Errors - Today	Errors - Past Week			

The details page displays:

- While the instrument is running, plate position information and ending time for a plate to finish its step is displayed.
- Remaining lamp life hours.
- Error log window tabs. Any reported errors for the current day and/or past week are retained inside these window tabs for your review.



Error logs

If needed, you can send instrument error logs to your support representative using your Thermo Fisher Cloud account or by emailing a zip file of your log files.

Using your cloud account

Using the email

option

1. Double-click on the **GCC Launcher** Desktop shortcut The Launcher window appears.



2. Double-click **Thermo Fisher Cloud Administration**. The Cloud Administration window appears.

IMPORTANT! Before accessing the cloud: a) You must have an active Internet connection. b) The **Enable Thermo Fisher Cloud Connectivity** check box must be checked.

- 3. Click the **Select Days** drop-down menu to choose the number of logged days you want to collect.
- 4. Click the **Upload Logs to Thermo Fisher Cloud** check box, then click **Gather Logs**. (Figure 18)

Figure 18 Generate and gather log files					
Generate Log Files Number of Days					
1	Upload Logs				
Select Days					
1					
2					
7					
14					

A percentage of completion wheel graphic appears (lower right), followed by a *Logs uploaded successfully* message.

5. Click **OK** to acknowledge the message.

The error log file(s) now reside on the cloud and are ready for your support representative to review.

1. Double-click on the **GCC Launcher** Desktop shortcut The Launcher window appears.

GCC	icon
GCC uncher	

- 2. Double-click **Thermo Fisher Cloud Administration**. The Administration window appears.
- 3. Click the **Select Days** drop-down menu to choose the number of logged days you want to collect. (Figure 19)

IMPORTANT! Before access The Enable Thermo Fisher Clo 3. Click the Selo

Figure 19 Generate and gather log files					
Generate Log Files Number of Days 1	Upload Logs to Thermo Fisher Cloud Gather Logs				
2 7 14					

4. Make sure the **Enable Thermo Fisher Cloud Connectivity** and **Upload Logs to Thermo Fisher Cloud** check boxes are unchecked, then click **Gather Logs**.

A percentage of completion wheel graphic appears (lower right). After a few moments, a message appears stating your logs have been collected and converted to a zip file on your Desktop. (Figure 20)

Figure 20 Logs collected message						
applied biosystems	Thermo Fisher Cloud Administration	_ □	×			
🗆 Enable Thermo Fisher	Cloud Connectivity					
Add User						
lf you do not have a Thermo l	isher Scientific account or forgot your password: CLICK HERE					
Connected Users	Thermo Fisher Cloud Registration ×		-			
User Name	Collected logs in file GCCLogs-06-24-2019 09-46-59.zip on					
Andy Irwin	the desktop.					
Delete User	ОК					
Generate Log Files						
Number of Days	Upload Logs to Thermo Fisher Cloud					
1	← Gather Logs					

- 5. Click **OK** to acknowledge the message.
- 6. Compose an email to your support representative, attach the Log Files zip file, then send the email as you normally would.



Uploading data manually

You can also manually upload your data results to your current cloud folder or subfolder, including failed data that has been successfully re-gridded and/or re-scanned.

IMPORTANT! Uploading data with unresolved scanning or gridding failures is not recommended.

Manually uploading data to the cloud

- 1. From the Data Connect web page, click \Lambda Upload files .
 - A Destination of files window appears. (Figure 21)

Figure	21 Data Connect	web page
=	DataConnect	Powered by Thermo Fisher Cloud 🔕 🙀 🚱 us 🚢
*	Manage and share your files an	nd projects Create a group 🚳 Upload files 💼 New folder Q D Previous versions 🛓 Download 🔿 Move 👔 Delete 🌧 Share
	~ m Recently Modified	File Name File Type Run Date Modified Date 🗸
*	 Personal Files 5504844340831 	550f X Destination of files X Where do you want to upload your files? Personal Files
	0% used 0 B of 10.0 GB	



Uploading a folder 1. Click Select Folder

A Browse for Folder window appears.

2. Navigate to your folder's location, click to highlight it, then click **OK**.

An **Uploading Files** status window appears (lower right), followed by a **Your files** have been uploaded window.

3. Click **X** to close this window.

Your manually uploaded folder and its contents now resides in your cloud folder. (Figure 21) To share the folder, see "Using the cloud to share data results".

Uploading a file 1. Click Select File.

An Explorer window appears.

2. Navigate to your file's location, click to highlight it, then click **Open**.

An **Uploading Files** status window appears (lower right), followed by a **Your files** have been uploaded window.

3. Click **X** to close this window.

Your manually uploaded file now resides in your cloud folder. (Figure 21) To share the file, see "Using the cloud to share data results".



Using the cloud to share data results

While connected to the cloud, you can share your uploaded data results.

1. Click the Data Connect icon.

The Data Connect window appears.

- From the folder list (left pane), click to select a data folder you want to share. Any applicable sub-folders appear.
- 3. Click to select the appropriate folder.

The middle pane populates.

4. From the middle pane, click to highlight the folder or file you want to share, then click the **Share with people** button. (Figure 22)

Figure 22 Data Connect web page										
=	DataConnect	Powered	by Thermo Fish	er Cloud ል				🔫 🚱 us	4 ~	
*	Manage and share your files and projects	S			2	· Create a group	🚯 Upload files	💕 New fold	er Q	
ē					C Previous vers	sions 🛓 Download	d 🔶 Move 🍵	Delete 🦂	Share	
	Recently Modified	File Name	File Type	Run Date	Modified Date 🗸	≠ 5500941111	1111111111111_(Axio	m_GW_Hu	×	
-	 Personal Files Genetitan Sample logs 	5500941111111111111111_Plate_Run_Summary_Report	TXT		08/Mar/2018		A Share with people	Ð		
		5500941111111111111111(Axiom_GW_Hu_SNP)_B02.A	AUDIT		08/Mar/2018	Data	Samples	Targets		
	✓ GTMC Log Samples	550094111111111111111(Axiom_GW_Hu_SNP)_B02.A	ARR		08/Mar/2018	Size:	3.3 KB			
	GeneTitanMC-Data	5500941111111111111111(Axiom_GW_Hu_SNP)_B02	JPG		08/Mar/2018	Updated by:	Updated by:	00/04	204.044	
	 Congoint Congoint<	550094111111111111111(Axiom_GW_Hu_SNP)_B02	CEL		08/Mar/2018	Run date:	06/Wai/2016 03.19.3	94 F WI		
		5500941111111111111111(Axiom_GW_Hu_SNP)_A01.A	AUDIT		08/Mar/2018	Data type:	ARR			
		550094111111111111111(Axiom_GW_Hu_SNP)_A01	JPG		08/Mar/2018	Owner:				
		5500941111111111111111(Axiom_GW_Hu_SNP)_A01	CEL		08/Mar/2018	Metadata			^	



Figure 23 Share window	
	×
Share	
To share with people, enter their email addresses separated by a comma between each email. Whe finished, press enter or click Add.	en
Add emails	Add
Shared with	
	Confirm

- In the Add emails field, enter the recipient's email address, then click Add. The email is now populated in the Shared with pane and is retained within the Add emails drop-down selection during your next session.
- 6. Click Confirm.

An email (with a hyper-link to your data) is sent to your recipient(s).

To delete an email/recipient from the Shared with list, click its adjacent **remove** option.



Portal and data organization

The data organization functions enable you to organize your data and copy files from place to place. The functions are described in:

- "Starting GCC portal", below
- "Viewing the data organization" on page 50
- "Searching for files" on page 66
- "Managing data roots" on page 75
- "Using projects to organize data" on page 78
- "Generating reports and summaries" on page 85
- "Copying files" on page 86
- "Specifying a default folder" on page 90
- "Uploading data to network data storage" on page 91

Disabling fast user switching

Fast user switching is an option in Windows that enables multiple active sessions on the console.

This option must be disabled on computers with GCC Portal installed, because it may cause a user to take actions under a different user ID and ultimately lock the first user from their data.

Refer to your Windows 10 Enterprise 2016 LTSB documentation on how to disable Fast user switching.

Starting GCC portal

- 1. Open the GCC Launcher.
- 2. Click GCC Portal.

The Home page appears. (Figure 24)



GCC portal home The GCC Home page (Figure 24) is your entry point to the GCC Portal functions. page



Home page features

- Menu Bar (see below)
- Search Functions (see "Searching for files" on page 66)



Home page	GCC Home PageWeb site and Support linksNetAffx Analysis Center
Data	 Folder View Project View Data Management functions (see Chapter 4, "Portal and data organization" on page 47).
Samples	 Sample Registration functions (see Chapter 5, "Creating and editing sample (ARR) files" on page 101).
Administration	 Project functions (see "Using projects to organize data" on page 78). Template functions (See "Working with templates" on page 328). Workflow Monitor (see "Tracking the workflow" on page 336).
Help	Online help
Tł	he Basic Search Function (Figure 25) enables you to search for files by:
	Array Name
	 Attribute value File Name

Project Name

Figure 25 Search co	ontrols			
	Select Search type	Enter search string	Click to start	search
Search Files By:	Array Name Array Name Array Name CLAttribute Value TRATION	N HELP	Use * for wildcard) 🧧	Advanced Search
	File Name Project Name			

For more information about the search options, see "Searching for files" on page 66.



Viewing the data organization

You have two different options for viewing the organization of data in GCC Portal:

- The Folder View displays a list of all the Data Roots in the GCC system, along with a list of the Sample, Data, and other files in a selected Data Root or sub-folder (see "Folder view" on page 50).
- The Project View displays the Sample and Data files associated with a selected project, showing parent and child relationships between the Sample and Data files (see "Project view" on page 63).

See "Organizing data" on page 32 for more information about the way data is organized in GCC.

Windows Security issues can impact your ability to view files and data. See Appendix B, "Windows sharing and security issues" on page 348 for more information.

Folder view The Folder View displays a list of all the Data Roots in the GCC system, along with a list of the content of a selected data root or sub-folder.

Using the folder view

1. Click View Folder View.

The Folder View appears (Figure 26).

The left side of the page displays the Folders list.

The right side displays the following items:

- Path to the selected folder
- Folder controls: used to open, add, and rename sub-folders
- Display controls: used to control the display of attributes and file types
- File List with Select controls: used to select files and perform operations on the selected files

Figure 26 Folder view							
Search Files By: 📓 🗛	ay Name 🔽	(Use * for wildcard)	<u>A</u>	vanced S	earch	0	
HOME DATA SAMPLES ADMINIS	TRATIO	N HELP					
Folders	Current l	Folder: C:\Command_Console\Data\Default 🔝 🗲	:				
B	Open	Add Subfolder Rename 🔶					
Build37EU133a [Build37EU133a]	View N	ew_View V (Customize) File filter Sho	v All	 Cust 	tomize	\leftarrow	
Default [Default]	67 Files		~	to Run	<select a="" com<="" th=""><th>manda V</th><th></th></select>	manda V	
Cancer [Cancer 2, Dr Moriarty]	122		Comman	a to Ixun			
Schizophrenia [Dr Monarty]	1 <u>23</u> <		Project	Lot			
Dr Watson Lab [Data]	Selected	File Name	Name	Number	Expiration	Array Name	Array Folder
Group			Default				
RealScanBuild647			Default				C:\Command_Console\Data\Default
		41/8/208-2896-4280-9889-615221/61690.AUDIT	Default				C:\Command_Console\Data\Default
⊕- C:\Command_Console\New_Root			Default				C:\Command_Console\Data\Default
		Sabe1 dag-2205-4bb-96b9-7abdobd2995 AUDI	Default				C:\Command_Console\Data\Default
		557379e2-33d3-4673-816d-814dd465arf0.4UDIT	Default				C:\Command Console\Data\Default
		5e7c9221-737c-4a98-ba06-9c1bdc4e2434.AUDIT	Default				C:\Command_Console\Data\Default
		80c640b1-82d5-4ddd-bee9-f208b8f783df.AUDIT	Default				C:\Command_Console\Data\Default
		@51059900405911030806400743887625.ARR	Default	4007438		@51059900405911030806400743887625	C:\Command_Console\Data\Default
	Г	■ @51059900405911030806400743887625.AUDIT	Default				C:\Command_Console\Data\Default
			Default	4007438		@51059900405911030806400743887625	C:\Command_Console\Data\Default
		■ @51059900405911030806400743887625.DAT	Default	4007438		@51059900405911030806400743887625	C:\Command_Console\Data\Default
		a @51059900405911030806400743887625.JPG	Default				C:\Command_Console\Data\Default
		@51068100251923030604300127464485.ARR	Default	3001274		@51068100251923030604300127464485	C:\Command_Console\Data\Default
		■ @51068100251923030604300127464485.AUDIT	Default				C:\Command_Console\Data\Default
	Γ	@51068100251923030604300127464485.CEL	Default	3001274		@51068100251923030604300127464485	C:\Command_Console\Data\Default
		@51068100251923030604300127464485.DAT	Default	3001274		@51068100251923030604300127464485	C:\Command_Console\Data\Default
		E)	Default				CulCommand, Console/Data/Default

The data roots and project folders are displayed in the Folders list (see below). The contents of the data roots and project folders are displayed in the File list (see "File list" on page 55).

For a description of the file hierarchy used to organize GCC files, see "Organizing data" on page 32.

The page links enable you to go to additional pages of data.

Figure 27 Folder view controls				
Current Folder: C:\Command_Console\Data\Dr Moriarty				
Open Add Subfolder Rename				
View Default V (Customize) File filter Show Affymetrix V (Customize)				
9 Files, 0 Selected Select All Unselect All Command to Run <select a="" command=""></select>				



Folders list

The Folders list (Figure 28) shows the data roots, folders, and projects used to organize data.



The Folders lists displays the folder names and project names for sub-folders.

Click on a folder to display its contents in the File list (see below).

The Folders controls enable you to:

- Add a folder (see "Adding folders and projects", below).
- Rename a folder (see "Renaming folders" on page 54).
- Open a selected folder in Explorer (see "Opening folders" on page 55).
 Note: You can add or rename a folder using Windows explorer in addition to the GCC Portal functions.

Adding folders and projects

You can add a new sub-folder in a selected data root or sub-folder using the Add Folder button. You can optionally assign the folder to a project of the same name when you create the folder.

- 1. Select the data root in the Folders list in which you want the new folder to be created.
- 2. Click the Add sub-folder button in the Folder controls (Figure 29).

Figure 29 Folder controls			
Current Folder: C:\Command_Console\Data\Dr Moriarty			
Open Add Subfolder Rename			
View Default View Customize File filter Show Affymetrix V Customize			
9 Files, 0 Selected Select All (Unselect All) Command to Run <select a="" command=""></select>			

The Add Subfolder window opens (Figure 30).

_

- 3. Enter the new folder name in the box.
- 4. Select the **Make folder and create project with same name** check box to create a project in GCC with the same name as the folder.
- 5. Click Add Folder.

The Folder View page opens with the new folder and project displayed.

Figure 31 New folder
Folders
□-/ Î C:\Command_Console\Data
🖶 🏧 Default [Default]
🖆 🔚 Dr Moriarty Lab [Dr Moriarty]
🖕 🔚 Dr Smith Lab [Dr Smith]
🚽 🛅 Dr Watson Lab [Data]
🖶 🦳 Alzheimer [Alzheimer 1, Data]
🗄 🔚 Hantavirus [Hantavirus, Data]
⊡-⊡Group



You can rename a folder using the Rename Folder link.

For information on changing the name of a project, see "Managing Projects" on page 78.

- 1. Select the folder to be renamed.
- Click the **Rename** button in the Folders controls (Figure 29). The Rename Folder page opens (Figure 32).

Figure 32 Rename Folder page					
Search Files By: 🛙 Array Name 💌 📃 (Use * for wildcard) 🧧 Advanced Search 🍳					
HOME DATA SAMPLES ADMINISTRATION HELP					
Rename Folder 🖻					
Rename folder C:\Command_Console\Data\HT_Test					
(Rename)					
Select the project to rename together with the folder					
OHT_Test					

3. Enter the new folder name in the box.

Select the radio button if you want to change the project name, too.

4. Click Rename.

The Folder View page opens with the renamed folder (Figure 33).



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Opening folders

- 1. Select the folder to be opened.
- 2. Click the **Open** button in the Folders controls (Figure 29).

An Explorer window opens displaying the contents of the folder. The GCC Portal browser shrinks to make room for the window (Figure 34).

C:\Command Console\Dat	a\Dr Moriarty			🖉 GeneChip Command Console Portal - Folder	Vie
File Edit Wew Favorites	Fools Help			Carlos - 🖉 http://localhost:8000/ - 49 🗙 💿	igle
A A	Court P	enter Do N	× n m.	Edit View Favorites Tools Help	
Greek , O , D	Disearch 10	roiders (3)	· · · · ·		
Address 🙆 C:\Command_Console\	Data\Dr Moriarty		*	V GR I Artymetrix GeneChip Com	· D · B · D Fade ·
Name	Size	Туре 🗠	Date Modified	Search Files By: 😫 Array Name 💌	
Cerebrum_03.CEL	5,250 KB	AGCC CEL File	1/30/2008 1:25 PM		
Cerebrum_03.DAT	58,177 KB	AGCC DAT File	1/30/2008 1:25 PM	HOME DATA SAMPLES ADMINIS	TRATION HELP
Cerebrum_03.ARR	4 KB	AGCC Sample File	1/30/2008 1:38 PM		
Dr_Smith_01.ARR	3 KB	AGCC Sample File	2/22/2008 4:02 PM	Folders	Current Folder: C:\C
Dr_Smith_02.ARR	2 KB	AGCC Sample File	2/22/2008 10:17 AM	E-C:\Command_Console\Data	(Open) Add Su
Dr_Smith_03.ARR	2 KB	AGCC Sample File	2/22/2008 10:21 AM	Batch Register Test (Batch Register Test	open Maa su
Moriarty_04.ARR	6 KB	AGCC Sample File	2/11/2008 5:00 PM	E-CEL and CHPAGC Cformat	
Moriarty_05.ARR	5 KB	AGCC Sample File	2/11/2008 5:00 PM		View Default
Cerebrum_03.AUDIT	40 KB	AUDIT File	1/30/2008 1:38 PM	Criecked_anes	
Dr_Smith_01_(HG-U133A_2)	5 KB	AUDIT File	2/22/2008 4:02 PM	Detault [Detault]	9 Files, 0 Selected (
Cerebrum_03.new.rma.chp	793 KB	CHP File	2/7/2008 12:53 PM	B Dr Moriarty [Dr Moriarty]	
Cerebrum_03.3PG	3,996 KB	JPEG Image	1/30/2008 1:25 PM	Drop_n_Scan [Drop_n_Scan]	Coloriad File Name
Dr Moriarty.PROJECT	1 KB	PROJECT File	1/30/2008 8:58 AM	- For_Rich	Selected File Name
probeset-summarize-2-7-12-5	6 KB	Text Document	2/7/2008 12:53 PM	B-ForDanoy 2	(C)
🗈 ma.summary.bit	371 KB	Text Document	2/7/2008 12:53 PM	Mito/2	line "
					Cerebrum
				or	Incorrect value
17 shisses		(7.0.10)	At Canadan	Reconnect_CEL_CHP [Reconnect_CEL_CHP	column "Age:
15 objects		67.0 MB	My Computer .:		data type is "

File list

The file list displays a list of the files and folders in the selected folder (Figure 35).

Figure 35 File List									
Current Folder: C:\Command_Console\Data\Default									
(Open) (Add Subfolder) (Rename)									
View Default V (Customize) File filter Snow V (Customize)									
31 Files,	0 Selected Select All Unselect All	Com	mand to Run <select a="" command=""></select>	×					
1 <u>2</u>							Decks		
Selected	<u>File Name</u>	Project Name	t <u>Array Name</u>	Barcode	<u>Lot</u> Number	Expiration Date	Array	Date Modified	
	&						Type		
	651059900405911030806400743887625.ARF	Default	@51059900405911030806400743887625	@51059900405911030806400743887625	4007438	3/8/2006	Test3_bens	7/13/2007 3:17:47 F	
	B51068100251923030604300127464485.ARF	Default	@51068100251923030604300127464485	@51068100251923030604300127464485	3001274	3/6/2004	HG-U133A	7/13/2007 10:37:22	
	@51068100251923030604300127464495.ARF	Default	@51068100251923030604300127464495	@51068100251923030604300127464495	3001274	3/6/2004	HG-U133A	7/13/2007 10:39:31	
	@51068100252003030704300131568507.ARR	Default	@51068100252003030704300131568507	@51068100252003030704300131568507	3001315	3/7/2004	HG-U133A	7/13/2007 10:43:46	File list
	051130200457544061306400949450147.ARF	Default	@51130200457544061306400949450147	@51130200457544061306400949450147	4009494	6/13/2006	E_coli_2	7/13/2007 10:11:14	
	052001900306143070204300292035858.ARF	Default	@52001900306143070204300292035858	@52001900306143070204300292035858	3002920	7/2/2004	HG- U133_Plus_2	7/13/2007 10:14:45	
	@52001900320743010605400001129266.ARR	Default	@52001900320743010605400001129266	@52001900320743010605400001129266	4000011	1/6/2005	HG- U133_Plus_2	7/13/2007 10:18:52	
	@52006500461817101306401416533696.ARF	Default	@52006500461817101306401416533696	@52006500461817101306401416533696	4014165	10/13/2006	HG-U133A_2	7/13/2007 10:28:42	
	@52006500461817101306401416533703.ARR	Default	@52006500461817101306401416533703	@52006500461817101306401416533703	4014165	10/13/2006	HG-U133A_2	7/13/2007 10:33:04	
	@52006500461817101306401416533707.ARF	Default	@52006500461817101306401416533707	@52006500461817101306401416533707	4014165	10/13/2006	HG-U133A_2	7/13/2007 10:30:54	
	First Sample.ARR	Default	First_Sample_array	@51068100252003030704300131568471	3001315	3/7/2004	HG-U133A	7/18/2007 5:32:02 F	
	851059900405911030806400743887625.CEL	Default	@51059900405911030806400743887625	\$\$\$1059900405911030806400743887625	4007438	3/8/2006	Test3_bens	7/13/2007 3:18:05 F	
	@51068100251923030604300127464485.CEL	Default	@51068100251923030604300127464485	@51068100251923030604300127464485	3001274	3/6/2004	HG-U133A	7/13/2007 10:37:42	

The Display controls, at the top, allow you to change the display of attributes and files. The select controls allow you to select files for various operations.



The numbered links below the Select controls enable you to switch from page to page of the File list. They are displayed only if the number of files in the selected sub-folder exceeds the display limit.

By default the File list displays a table of files with the following columns:

Select	Use the check box to select a file for different operations:
	 Copy Selected Files (see "Copying files" on page 86).
	Create Report from Sample files in List (see "Copying files" on page 86).
	Change Probe Array Type (see Chapter 10, "Probe array types" on page 325).
	See "Selecting files" on page 57 for more information.
	Placing your cursor over the Select check box displays the full path and file name in a popup:
	© <u>@51068100251923030604300127464495.ARR</u> Default @5106810 C:\Command_Console\Data\Default\@51068100251923030604300127464495.ARR}1(
FileName	The name of the file or folder.
	In some cases the file name is a link. Click on the link to open the following file types:
	 Folder: displays the contents of the folder in the file list.
	 Sample File: opens the Sample/Array Attributes page (see "Detailed sample registration" on page 104).
	• Image file (DAT) and Intensity File (CEL): opens the GCC Viewer (see Chapter 9, "Using the GCC viewer" on page 267).
	• Audit file (AUDIT): opens the Audit File Viewer (see "Viewing audit files" on page 65)
	You cannot use the Action link to open the other file types displayed in the File list. These file
	types can be opened using a text editor (AUDIT, RPT, GRD) or the GCC Viewer (CEL, JPG).
Project Name	The name of the project that contains the file.
Array Name	Name assigned to the array during registration.
Barcode	Barcode of probe array (may be an Applied Biosystems or a custom barcode).
Lot Number	Manufacturer's lot number for the array (only displayed with Applied Biosystems barcodes).
Expiration Date	Expiration date for the array (only displayed with Applied Biosystems barcodes).
Probe Array Type	Model number of probe array.
Date Modified	Last date the file was modified.

You can conceal some of these columns and display selected attributes in other columns. For information about displaying and concealing columns, see "Selecting attributes for the file list" on page 57.

Sorting the file list by any column

• Click on the column header.

File types

There are several different types of files in the File List:

- Sample files (ARR)
- Image files (DAT)
- Intensity Data Files (CEL)

- Probe Analysis Files (CHP)
- JPG files (JPG)
- Audit Information files (AUDIT)
- Grid Data files (GRD)
- Project files (PROJECT)
- Report files (RPT)

For more information about the different files, see "File types in GCC" on page 28.

See "Selecting file types for display" on page 61 for more information about displaying different file types.

Note: Other file types, such as PARAM, may not be displayed in the list or the folders.

Selecting files

You can use the check boxes in the File list to select files for different operations:

- Copy Selected Files (see "Copying files" on page 86).
- Create Report from Sample files in List (see "Generating reports for selected sample files" on page 85).
- Create Batch Edit file from Selected ARR Files in List (see "Creating the batch edit file" on page 145).
- Change Probe Array Type (see Chapter 10, "Probe array types" on page 325).

Figure 36 Select Files controls						
2 Folders, 16 Files, 0 Selected Select	All Unselect All Command to Run (Select a command>	~				
Selected File Name	Project Name Array Name	Date Modified				

The Select Files controls allow you to select files and operations. The number of displayed and selected files are also displayed.

Selecting/Deselecting files

- Click the check box next to the file name; or click the Select All button.
- Click the Unselect All button to deselect selected files.

Selecting attributes for the file list

You can add or delete attributes for display in the File List using the Folder View feature. The Folder view enables you to create and edit lists of attributes to be displayed, called views. You can then select a view for display to customize the attributes in the File list.

Note: When cartridge users upgrade, the default folder view does not have well position (Pos) in the default folder view. If they have GeneTitan Array Plate data and want to see this attribute in the folder view, they will either need to add it to the default folder or create a custom view with that attribute. The Pos attribute is part of the standard fields.

Selecting a previously created view

• In the File controls, Click the View drop-down to select a view. (Figure 37)

Figure 37 File list with View controls					
View New_View Customize File filter S	thow All Customize				
66 Files, 0 Selected Select All Unselect All	Command to Run <select a="" command=""></select>				
1 <u>2</u> 3					
Selected File Name	<u>Project Lot</u> <u>Name</u> <u>Number</u> <u>Expiration</u> <u>Array Name</u>				

The selected View is displayed.

Adding a new view

1. Click the View Customize button. (Figure 37)

The Customize page opens. (Figure 38)

Figure 38 Add New Folder	View page		
HOME DATA SAMPLES ADMINISTRA	TION HELP		
Enables users to choose the attributes displayed in Users can store several different views containing diff	he folder and search result views. erent collections of attributes.		
Step 1: Create a new view (Optional) New view name:	Add		
Step 2: Select the view to modify Select existing view: Default V			
Step 3: Select the source of attributes Attributes Source Attributes From All Templates Attributes From Selected Templates Standard Fields User Attributes Step 4: Select the attributes Double click on a field to add it at the end of the ot Save Cancel	Template ample Information nplate_12_06 mplate her list or Drag and Drop it to the desired lo	cation.	
Available Attributes Sorted Array Folder Date Created Sample Name:Default Gender:Default Weight:Default Height:Default	Add All attributes Remove All attributes Add all attributes of template(s) below Default	Displayed Attributes File Name Project Name Array Name Date Modified	

There are three steps in creating a new view:

- a. Enter a name for the view.
- b. Select the source of attributes.
- c. Select the attributes and saving the view.
- 2. Enter a name for the view in the New View Name box and click the **Add** button. (Figure 39)

Figure 39 New View Name					
Step 1: Create a new view (Optional)					
New view name:	Add				

The view name is displayed in the Select Existing View drop-down box. (Figure 40)

Figure 40 New view name in the Select Existing View drop-down box.			
Step 2: Select the view to modify Select existing view: New_View V			

In this step, you select the sources of the attributes. (Figure 41)

Figure 41 Select Source controls	
Step 3: Select the source of attrib Attributes Source	outes
C Attributes From All Templates Attributes From Selected Templates Standard Fields User Attributes	asdfwe DEC Exp Template Default fdfsa Ihg MIAME Sample Information New_Template_12_05 Sept_Template

You have several options for doing this:

- You can limit the display to attributes that are organized in templates.
- You can display user attributes which have been created by the user for individual sample files.

- If you want to use standard fields, you can display the fields from all templates, or display attributes from templates you select in the Attributes Source list.
- 3. Select the attributes options and templates

The selected attributes are displayed in the Available Attributes list.

- The **Available Attributes** list displays the attributes (with template names) that are not being currently displayed.
- The **Displayed Attributes** lists displays the attributes that are currently being displayed in the Folder view.
- The File Name attribute is required and cannot be hidden.
- 4. Select and deselect the items you want to display and conceal.
 - You can double-click on an item in one of the lists to move it to the other list or click and drag it over.
 - You can also use the center controls to add and remove attributes in groups.
 - Select the Sorted check box to display the available attributes in alphabetical order.
- 5. After selecting the attributes, click **Save**.

The Folder View is displayed with the newly created view selected in the View drop-down box.

Editing a created custom view

1. Click the View Customize button.

The Customize page opens.

 Select the view you want to edit from the Select existing view drop-down box. (Figure 42)

You can click the **Delete** button to delete the selected view.

Figure 42 Selecting existing view to edit			
Step 2: Select the Select existing view:	view to mo New_View 👽 Default New_View	dify Delete	

The attributes in the view are displayed in the Select Attributes section. (Figure 43)

Figure 43 Selec	ting attributes	
Figure 43 Select	ibutes ibutes Id it at the end of the other list or Drag and Drop it to the desir ise orted Add All attributes Add All attributes Add all attributes Add all attributes Default Below Default Below Carter Carte	ed location. Displayed Attributes File Name Project Name Array Name Array Folder Gender:Default Age:SeptTemplate Disease name:SeptTemplate Disease status:SeptTemplate Treated:*

- 3. Select templates and attributes as described on page 58.
- After you have selected and arranged the attributes, click Save. You can click Cancel to cancel the changes.
- 5. The View is displayed in the Folders list with the new attributes selected.

Selecting file types for display

The File Filter enables you to exclude or include particular file types in the File list. You can:

- Use a previously created filter
- Create a new file filter.
- Edit a previously created filter

Using a previously created filter

• In the Filter controls, select the File filter from the drop-down list.

Figure 44 Folder list with File Filter controls
View New_View V Customize File filter Show All V Customize Show Affymetrix Show Affymetrix
66 Files, 0 Selected Select All (Unselect All) Command to Run (Select a command)

The filtered files are displayed.

Creating a new file filter

1. In the top of the File list, click the File Filter Customize button (Figure 45).

Figure 45 Folder list with File Filter controls
View New_View View Customize File filter Show All Customize Customize
66 Files, 0 Selected (Select All) (Unselect All) Command to Run «Select a command»

The File Filters page appears (Figure 46).

Figure 46 File Filter page		
Search Files By: Array Name V	(use * for wildcard suffix) 2 Advanced Set	arch
File Filters		
Step 1: Enter a new filter name and click Add. New Filter: Add		
Step 2: Select File Types for the Filter File Type(s): • ARR; * CEL; * DAT; * CHP Delete	Filter Type: III	
	Save Cancel	

- 2. Enter a name for the new filter in the new Filter list.
- 3. Click Add.

The new filter name appears in the Name box.

Enter the file types you want to exclude or include in the Patterns box.
 Format: *.file extension, (* = wildcard).

Enter multiple file types separated by semicolons (;).

- 5. Select whether you want to exclude or include the specified file types.
- 6. Click Save.

The Folder View appears with the edited filter selected. The displayed files are filtered.

Editing a file filter

1. In the top of the File list, click the **Customize** button (Figure 44).

The File Filters page appears (Figure 47).



		Search	Files By: Ana	y Name 🔽		(use * for wildo	ard suffix) 🔛	Advanced S
HOME DATA SAMPLES A	ADMINIS	TRATION HEL	P					
File Filters 💷								
Step 1: Enter a new filter name	and click A	dd.						
New Filter:		Add						
							_	
Step 2: Select File Types for the F	ilter							
Filter Name: 💷 Show Attymetrix	~	File Type(s): 🛄 *	.ARR; *.CEL; *.E	AT; *.CHP	Filter Type: 📕	Including		
Delete								
Delete								
					Save	Cancel)	

- 2. Select the filter you want to edit from the Filter Name drop-down list.
- Enter the file types you want to exclude or include in the Patterns box.
 Format: *.file extension, where * is a wildcard.
 Enter multiple file types separated by semicolons (;).
- 4. Select whether you want to exclude or include the specified file types.
- 5. Click Save.

The Folder view appears with the edited filter selected. The displayed files are filtered.

Project view The Project View displays the Sample and Data files associated with a selected project, showing parent and child relationships between the Sample and Data files:

- Array name(s)
- Image (DAT) file(s)
- Intensity Data (CEL) file(s)
- Probe Level Summarization (CHP) file(s)

The Project view also displays basic information about a selected file, and will allow you to open and view Sample, DAT, and CEL files.

Viewing the Sample and data files associated with a project

1. Click View \rightarrow Project View.

The Project View pages opens.

2. Select a project from the Project list.

A list of the Sample files associated with that project is displayed. (Figure 48) You can expand the file structure by expanding and contracting nodes in the tree.

Figure 48 Project view page with sample files list				
Search Files By: Array Name	V (Use * for wildcard) Advanced Search			
HOME DATA SAMPLES ADMINISTRAT	FION HELP			
Project View 🖬				
The Project View displays the files associated with a p the sample file and the array(s), the Image (DAT) files Project: Attheimer 1 3 Arrays:	articular project. The view displays basic information about the Sample (ARR) file and the relationships between (s), the Intensity Data (CEL) file(s) and the Probe Level Summarization (CHP) file(s) 0 files selected Select All Unselect All Command to Run Celect a command Associated projects: Alzheimer 1, Data File Details Full Path: C:\Command_Console\Data\Dr Watson Lab\Alzheimer\ALZ_01.ARR Open Arrays Barcode Probe Array Type Array Name @\$1059900413526052906400976113289(Lot# 4009761, Exp. 5/29/2006) Test3 ALZ_01_PL_01_A_1 @\$1059900413526052906400976113286(Lot# 4009761, Exp. 5/29/2006) Test3 ALZ_01_PL_02_A_1			

3. Click on a file to display more information about the file in the right side of the page.

Different information is displayed for different files, as shown in Figure 49.

Figure 49 In	nformation for selected CEL fi	le				
Associated proje	Associated projects: Dr Smith					
File Details						
Full Path:						
C:\Command_Console\Data\Dr Smith Lab\Subject_01_brain.CEL Open						
Date Modified:	Date Modified:					
6/20/2007 4:33:08 PM						
Parameter	Value					
algorithm name	Feature Extraction Cell Generation					
algorithm version	1.0.0.610					
array type	Test3					
array barcode	@51059900309137041705400091668927					

- 4. For certain files, you can click the Open button to display the file:
 - Sample files: Opens the Detailed Registration Page (see "Detailed sample registration" on page 104).
 - DAT and CEL files: Opens the GCC Viewer (see Chapter 9, "Using the GCC viewer" on page 267).

Selecting files

You can use the check boxes in the Project data tree to select files for different operations:

- Copy Selected Files (see "Copying files" on page 86).
- Create Report from Sample files in List (see "Generating reports for selected sample files" on page 85).
- Create Batch Edit file from Selected ARR Files in List (see "Creating the batch edit file" on page 145).
- Change Probe Array Type (see Chapter 10, "Probe array types" on page 325).

Figure 50 Select Fi	les controls			
]
6 files selected	Select All	Unselect All	Command to Run	<select a="" command=""></select>

The Select Files controls allow you to select files and operations. The number of selected files are also displayed.

Selecting files

- 1. Click the check box next to the file name; or
 - Click the Select All button.

Click the **Unselect All** button to un select selected files.

When you select a parent file, all its child files are also selected. If you only want to select the parent file, deselect its child files after selecting the parent file.

2. Select an operation from the **Command to Run** drop-down.

Viewing audit files Audit files provide a record of the processing done to an array.

Opening an audit file

- 1. Click on the link in the File List
- 2. The Audit File page opens. (Figure 51)



Figure 51 Audit File page
Saarah Filas Bur Arry Huma V (use * for wild and with)
HUME DATA SAMPLES ADMINISTRATION HELP
Audi File Caconintanu_ConsoleData/aaa2502a-/400-4010-6015-10/414/05426.AOD11
Audit Entry
Array ID aaa53d9a-74cd-4dfb-8ef9-f074147b5498
Bar Code
Source
Bar Code
Insertion Params
System Entry
Domain Name AFFYMETRIX_COM
User Name SYSTEM
Machine Name XPLCC4Y9851
Audit Entry
Array ID aaa53d9a-74cd-4dfb-8ef9-f074147b5498
Bar Code
Surge
Bar Code
Insertion Params
System Entry
Domain Name AFFYMETRIX_COM
User Name SYSTEM
Machine Name XPLCC4Y9851

The Audit File displays information about the processing steps the array has gone through, including the instruments and computers used in processing.

Searching for files

You have two options for locating files in GCC:

- "Basic search", below
- "Advanced search" on page 67

The results are displayed in the Search Results page (see "Search results page" on page 74).

Note: Windows Security issues have an impact on the search function. for more information, see Appendix B, "Windows sharing and security issues" on page 348.

Basic search The Search Function (Figure 52) enables you to search for files by:

- Array Name
- Attribute Value

Note: Searching by Attribute Value returns any file with any attribute with a value that matches the search string. To search for a particular attribute, use the Advanced Search.

- File Name
- Project Name

Figure 52 Search controls		
		Olialista atast
Select Search type	Enter search string	Click to start
Search Files By: 🛙	Array Name 😽	
HOME DATA SAMPL	Array Name Attribute Value TRATIC	ON HELP
	File Name Project Name	

Searching for a file

- 1. From the Search Files By drop-down list, select your search criteria.
- 2. Enter a search string in the text box.

You can perform special searches by using the "*" symbol and "OR" operator

"*" Serves as a wild card function. Using searchstring* will return all
arrays that contain an attribute that starts with the search string. Using
*searchstring will return all arrays that contain an attribute that ends with
the search string.

Using the "OR" operator between items (searchstring1 OR searchstring2) will return all arrays that contain an attribute that matches any of the search strings.

3. Click the **Search** button **I**.

Files or Projects that match the search string are displayed in the Search Results page (see "Search results page" on page 74).

Advanced search The Advanced search provides several ways to refine your search.

1. Click **Advanced Search** in the Search controls.

The Advanced Search page opens. (Figure 53)



Figure 53	Advanced Search page
	Search Files By: Array Name (Use * for wildcard) Advanced Search (Use * for wildcard) Advanced Search (Use * for wildcard)
	Advanced Search
Array Search	Step 1: Specify the array search criteria
Criteria	Probe Array Types: All Probe Array Types Barley1 E_coil_2 HG-U133_Plus_2 V Array Name:
	Step 2: Specify sample attributes to filter the search results
Sample Attributes	Select Template Select Attribute Select Comparison Enter Value(s) Select template V (Select template first) V Delete Add
	e Results must match ALL of the selected attributes C Results can match ANY of the selected attributes
	Step 3: Specify options to limit the search results
Options	Type of results to Limit results to the Projects: Only return files whose return: ABR DAT CEL CHP Only return files whose Cancer 1 Cancer 2 Only return files whose Cancer 4 C
	Show all Search Search

You create a search in three steps:

- "Step 1: Specify Array Search Criteria"
- "Step 2: Specify Sample Attributes" on page 69
- "Step 3: Select Options" on page 72

Step 1: Specify Array Search Criteria

Figure 54 Array Search Criteria				
Step 1: Specify the array	arch criteria			
Probe Array Types:	Barcode:			
Barley1 E_coli_2				
HG-U133_Plus_2	MIIAY IVAILIE.			

This section enables you to search for arrays that match:

- Barcode
- Probe Array Type
- Array Names
- 2. Enter the criteria for the information you want to find.

Step 2: Specify Sample Attributes



This section (Figure 55) enables you to specify attributes used to describe the sample and experiment. Depending upon how the search is set up, the search may return:

- Samples with any of the specified attributes.

- Samples that match all of the specified attributes.

Four things have to be selected or entered to specify an attribute:

- the source of the attribute (template name or user attribute)
- the attribute name
- the type of comparison
- the value for the attribute

When the Advanced Search page first opens, the sample attributes has three drop-down lists:

- Select Template
- Select Attribute
- Select Comparison

The Enter Value(s) box does not appear until you have selected a template and attribute.

To select an attribute:

3. From the Select Template drop-down list, select a template or other option.

Note: The Sample Attribute Conversion function may impact your selection of templates and attributes. For more information, see "Sample attributes conversion" on page 115.

The Select Template list displays a list of the templates used by the files in GCC. You can also select:

• All attributes: Enables you to perform a blanket search over every attribute in the Sample files, both from templates and from user attributes.

See "Performing an all attributes search" on page 74 for more information.

 No Templates: Enables you to select from user attributes, used in a Sample file but not included in a template.



Figure 56 Selecting	a template			
Step 2: Specify sample attributes to filter the search results				
Select Template	Select Attribute Select Comparison Enter Value(s)			
Select template 🛛 🗸	(Select template 💙 (Select template first) 🗸			
Select template All Attributes	Add			
No Template DEC Exp Template Default MIAME Sample Inforr Sept_Template	atch ALL of the selected attributes atch ANY of the selected attributes			

4. After selecting the template, a list of attributes appears in the Select Attributes drop-down list. (Figure 57)

Figure 57 Select attribute from list	
Step 2: Specify sample attributes to filter the search results	
Select Template Select Attribute Select Comparison	Enter Value(s)
Sept_Template V Disease name V Equal to:	(use * for
Delete A Disease name Disease status	
• Results must match ALL of the selected attributes	
C Results can match ANY of the selected attributes	

5. Select the attribute you want to search on.

You can perform different types of comparisons for the search.

If you select a numerical attribute, you can select from the following limits (Figure 58):

- Equal to
- Less than
- Less than or equal to
- Greater than
- Between (displays two entry boxes for the range limits).
- Any value

- 10		74	
	\sim	61	
\sim	7.	41	
	r A		
	_		-
- 100			

Figure 58 Comparisons for numeric	al attributes	
Step 2: Specify sample attributes to f	filter the search result	S
Select Template Select Attribute S	Select Comparison	Enter Value(s)
 Sept_Template Age Delete Add Results must match ALL of the select Results can match ANY of the select 	Equal to: Equal to: Less than: Less than or equal to: Greater than: Greater than or equal to: Between: Any value	

For date attributes, the comparisons are:

- Equal to today
- Within the last week
- On a specific date: (required)
- Before date: (required)
- After date: (required)
- Between dates: (required)
- Any value

For text string or SingleSelect attributes, the comparisons are (Figure 59):

- Equal to: exact match to the search string
- Contains: text string containing the search string

Figure 59 Comparisons for text string attributes	
Step 2: Specify sample attributes to filter the search results	
Select Template Select Attribute Select Comparison	Enter Value(s)
🔽 Sept_Template 💌 Age 💉 Greater than: 💌 18	
🔲 Sept_Template 💙 Disease status 💟 Equal to: 💙	(use * f
Delete Add Equal to: Contains:	
Results must match ALL of the selected attributes	
C Results can match ANY of the selected attributes	

6. Select the appropriate comparison for the attribute.

You can use comparisons with user attributes that have the data type specified, as well as sample attributes.

7. Enter a string for the attribute in the Enter Value(s) box.

You can perform special searches by using the "*" symbol and "OR" operator when searching for Text attributes.



Note: [*] serves as a wild card function. Using searchstring* will return all arrays that contain an attribute that starts with the search string. Using *searchstring will return all arrays that contain an attribute that ends with the search string.

Using the "OR" operator between items (searchstring1 OR searchstring2) will return all arrays that contain an attribute that matches any of the search strings.

For date attributes, click on the Calendar icon in and select the date from the calendar that appears. (Figure 60)

Figure 60 Selecting dates							
Step 2: Specify sample attributes to filter the search results							
Select Template Select Attribute Select Compa	risc	n	Er	ıter	Val	lue(s)
🔲 No Template 🛛 🔽 Sample Date 💟 On a specific date		~ .	lul 1	1 2	nnz		
Delete Add	Su	Mo	Jui	y Zu We	JU Z Th	Fr	Sa
	1	2	3	4	5	6	7
Results must match ALL of the selected attributes	8	9	10	11	12	13	14
C Results can match ANY of the selected attributes			17	18	19	20	21
		23	24	25	26	27	28
Step 3: Specify options to limit the search results	29	30	31	1	2	3	4
Type of results to Limit results	5	6	7	8	9	10	11

Click the < and > buttons to display a different month.

- 8. Click the Add button to add another attribute and repeat Step 3 through Step 7.
- 9. Select how the searches are to be combined:
 - Results must match ALL of the selected attributes.
 - Results can match ANY of the selected attributes.

After you have finished specifying the attributes, you can select other options.

Step 3: Select Options

Figure 61 Options for limiting search results					
Step 3: Specify options to limit the s	earch results				
Type of results to return: ARR DAT CEL CHP	Limit results to the Projects: - All Projects and Data Roots Alzheimer 1 Build37EU133a Cancer 1 Cancer 2	Only return files whose creation dates are: Any value			
Show all 💌 results	Search				

This section enables you to search for files that match other criteria:
Type of results Specify one or more of the following types of files: to return

- ARR
 - CEL
 - CHP
 - DAT

Limit results to Projects to be searched. Selecting none runs the search through all the files in the the Projects main data folder and in all the project folders. You can limit your search to one or more project folders using this box.

Creation Dates Date of file creation:

- Equal to today
- Within the last week
- On a specific date: (requires date value)
- Before date: (requires date value)
- After date: (requires date value)
- Between dates: (requires date value)
- Any value

Show results Limit on the number of results to be returned.

10. Select or enter the options for the information you want to find.

You can select multiple items in the Type of Results and Projects list by holding down the Shift key and clicking on the items.

You can deselect a project by holding down the Ctrl key and clicking on the project.

For date attributes, click on the Calendar icon 📰 and select the date from the calendar that appears. (Figure 62)

Figure 62 Select date								
Only return files wh	ose	crea	atio	n da	tes	are:		
Before date: 🗸 🗸								Ĩ
	•		Jul	y 2(07		•	
	Su	Мо	Tu	We	Th	Fr	Sa	L
	1	2	3	4	5	6	7	L
	8	9	10	11	12	13	14	L
	15	16	17	18	19	20	21	L
	22	23	24	25	26	27	28	L
	29	30	31	1	2	3	4	L
	5	6	7	8	9	10	11	L
								1

Click the < and > buttons to display a different month.

11. Click Search.

The files that match the search criteria appear in the Search Results list.

Performing an all attributes search

The **All Attribute** search enables you to search across all attributes of the following types:

- Date
- Number
- Text

If you use the All Attributes search, it will return any file that has any attribute with a value that matches the search string.

Search results page

The Search Results page lists the files that meet the criteria specified in your search. (Figure 63)

Figure 63 Search Results list		
[
Search Files By: Array Name 💌	(Use * for wildcard) 🔤 Advanced Search	۹
HOME DATA SAMPLES ADMINISTRATION HELP		
Search Result 😰		
View New_View V Customize		
2 Files, 2 Selected Select All Unselect All Command to Run (Select a c	oommand>	
Selected File Name Project Name Array Name Array Folder	Gender:Default Age:Sept Template	Disease nt Tomplete status Sent Tomplete Treated: *
Subject 01 brain.ARR Dr Smith Subject_01_brain Smith Lab	^{Dr} M 25 schizophre	nia Y No
Subject 02 brain.ARR Dr Smith Subject_02_brain C:\Command_Console\Data\C	Dr F 40 Depression	n Y No

You can:

- Change sort order of the list by clicking at the head of the column you want to sort by.
- Change the attributes displayed in the list with the View controls (see "Selecting attributes for the file list" on page 57).
- Use the Select controls to select files for various operations.

Placing your cursor over the Select check box displays the full path and file name in a popup (Figure 64):

Alzheimer ALZ_02_ARR Alzheimer ALZ_02_
N2
C:\Command_Console\Data\Dr Watson Lab\Alzheimer\ALZ_02.ARR





Selecting files

You can use the check boxes in the Selected column to select files for different operations:

- Copying Selected Files to a different location (see "Copying files" on page 86).
- Create Report from Sample files in List (see "Generating reports for selected sample files" on page 85). The Report can be used to review the file attributes.
- Create Batch Edit file from Selected ARR Files in List (see "Creating the batch edit file" on page 145)
- Change Probe Array Type (see Chapter 10, "Probe array types" on page 325).

Figure 65 Select Files controls	
2 Files, 2 Selected Select All Unselect All	Command to Run <select a="" command=""></select>

The Select Files controls allow you to select files and operations. The number of selected files are also displayed.

1. Click the check box next to the file name; or

Click the Select All button.

Click the Unselect All button to unselect selected files.

2. Select an operation from the **Command to Run** drop-down.

Managing data roots

A data root is a folder used to contain data files for GCC. The folder and files are displayed in the Folder View of Command Console. A default data root at C:\Command_Console\Data is created during installation, but you can create additional data roots to help you organize data from different researchers or for other purposes.

IMPORTANT! Each workstation has its own data roots. Setting the data root on one station does not add the data root on other machines.

IMPORTANT! Please make sure that the data roots used in GCC software on the instrument control workstations do not contain files that have non-Thermo Fisher Scientific file extensions (example: DLL, TMP, CPP, ASPX, OUT, etc).

For more information about data roots, see "Folders" on page 32.

You can:

- Create a data root (see "Adding a data root", below)
- Remove a data root (see "Removing a data root" on page 77)

Adding a data root

1. From the Data menu, select **Data Roots Add**.

The Add Data Roots page opens (Figure 66).

Figure 66 Data Root pa	age		
HOME DATA SAMPLES A	Search Files By: Array Name 💌	(use * for wildcard suffix) 🖻	Advanced Search
Add Data Root			
Data Reveis Col: Col: Col: Col: Available folders Col: Available folders Col: Archive Calvin_Configurations Calvin_Configurations Calvin_Configurations Calvin_Configuration Calvin_Configuration Command_Console Configuration Configuration	New data root C:\Command_Console\More_Data	Add	

The Data Root page displays a list of the data roots currently assigned in GCC and the folders that can be selected as data roots. Expand the tree to view and select child folders.

2. Select a folder for the new data root from the Data Root list; or

In the **Add a New Data Root** box, enter the full path name and the name of the new data root.

Data roots on networked computers are specified using Universal Naming Convention (UNC) paths as \\server\share\filepath.

IMPORTANT! To select a data root on a networked computer, you must configure the GCC Services to permit access. See "Configuring GCC services" on page 344 for more information.

IMPORTANT! Please make sure that the data roots used in GCC software on the instrument control workstations do not contain files that have non-Applied Biosystems file extensions (example: DLL, TMP, CPP, ASPX, OUT, etc).

The folder cannot be:

- In the Windows directory
- In the Program Files directory
- In a root directory



3. Click Add.

The list displays the new data root (Figure 67).

Figure 67 New data root added
Figure 67 New data root added Search Files By: Arry Name (use * for wildcard suffix) Advanced Search HOME DATA SAMPLES ADMINISTRATION HELP Add Data Root Data Root Added new data root C:\Command_Console\More_Data Added new data root Added new data root Added new data root Added new data root New data root Added Added new data root Added

The new data root is also visible in the Folder View (see "Folder view" on page 50).

Removing a data root

1. From the Data menu, select **Data Roots Remove**.

The Remove Data Root page opens (Figure 68).

Figure 68 Remove Data Root page	
<u>k</u>	
Search Files By: 🔟 Array Name 💌 (Use * for wildcard) 🛂 Advanced Search	٩
HOME DATA SAMPLES ADMINISTRATION HELP	
Remove Data Root 🗵	
Select the data root that you wish to remove from the system. The data will not be deleted. The system will no longer allow samples to a registered to this location and data in removed data roots will not be returned in search results. Data root 'C:ICommand_Console:Data' contains Default System Folder 'C:ICommand_Console:Data:Default' and cannot be deleted. It change Default Folder Available Data Roots C:ICommand_Console:Data2 C:ICommand_Console:New_Root Remove	re f you

The Remove Data Root page displays a list of the data roots available to GCC.

Note: You cannot delete the default data root. You must assign default status to another data root before deleting the current default data root. For more information, see "Specifying a default folder" on page 90.

- 2. Select the radio button next to the data root.
- 3. Click **Remove**.

IMPORTANT! Deleting a data root in GCC does not delete the actual root directory or data files in Windows.

Using projects to organize data

A project is a label assigned to a Data Root or sub-folder that can be used to organize Sample and data files. If you assign a project name to a Data Root or sub-folder, all the Sample and data files in that folder are assigned that project name. Any child subfolders of that project folder are assigned the project name, as well. A project name can be assigned to multiple Data Roots or sub-folders, in order to group data on multiple folders together.

Project folders enable you to organize your data. After organizing data into projects you can:

- Display data grouped by project
- · Search on data limited to a project
- Create a spreadsheet listing the Sample (ARR) files assigned to the project. The list can be reviewed as a summary of the project information or used to edit the Sample (ARR) file content using Batch Edit.

The Projects functions provide tools for:

- "Managing Projects"
- "Copying files"

Managing Projects

Opening the Manage Projects page

• From the Administration menu, select **Project Manage**. The Manage Projects page opens (Figure 69).

ojects to organize data	4

Figure 69 Manage Projects pa	age
Search Files By: Array Name	(Use * for wildcard) 2 Advanced Search
HOME DATA SAMPLES ADMINISTRATI	ON HELP
Folders	Create New Project 🚨
G-fillC:\Command_Console\Data	Select where you would like the project to go by clicking on the tree view on the left.
	Create new project Cancer in the 'C:\Command_Console\Data\Dr Smith Lab\Cancer' folder
Cancer [Cancer 1, Dr Smith]	Create subfolder in the 'C:\Command_Console\Data\Dr Smith Lab\Cancer' folder
Group	Manage existing projects 🖻
שישיאנג (אטגג)	Select Project: Acheimer 1
	Delete project name. This deletes the project name only. The data and folders are not deleted.
	Root folders in the 'Alzheimer 1' project
	Add 'C:\Command_Console\Data\Dr Smith Lab\Cancer' folder to the 'Alzheimer 1' project
	Folder Primary Delete
	C:\Command_Console\Data\Dr Watson

The page has a folders list on the left side, similar to the one in the Folder View page.

The work area on the right has controls that allow you to:

- Create a new sub-folder.
- Assign a project name to a folder.
- Designate a primary folder for a project.
- Add or delete folders for a project.

Creating a project

The Create New Project controls of the Manage Projects page enables you to:

- Assign a previously created Data Root or sub-folder to a project
- Create a sub-folder and assign it to a project.

Figure 70 Create New Project controls	
Create New Project 😰	
Select where you would like the project to go by	clicking on the tree view on the left.
Create new project	in the 'C:\Command_Console\Data' folder
Create subfolder	in the 'C:\Command_Console\Data' folder

Creating a sub-folder and project

- 1. From the Administration menu, select **Project Manage**.
 - The Project Management page opens. (Figure 71)

Figure 71 Manage Projects pa	age
Search Files Ry: Anav Name	(The * for wildowd) D Advanced Search
HOME DATA SAMPLES ADMINISTRATI	
Folders C:Command_Console\Data G:Default [Default] D:Default [Default] D:D:Smith Lab [Dr Smith] D:D:Smith Lab [Default] D:D:Smith] D:D:Smith]	Create New Project Select where you would like the project to go by clicking on the tree view on the left. Create new project Cancer in the 'C:\Command_Console\Data\Dr Smith Lab\Cancer' folder Create subfolder in the 'C:\Command_Console\Data\Dr Smith Lab\Cancer' folder Manage existing projects Select Project: Atcheimer 1 Celete project name. This deletes the project name only. The data and folders are not deleted. Root folders in the 'Alzheimer 1' project Add 'C:\Command_Console\Data\Dr Smith Lab\Cancer' folder to the 'Alzheimer I' project Folder Primary Delete C\Console\Data\Dr Watson C\Command_Console\Data\Dr Watson

2. In the Folders tree, select the Data Root or sub-folder where you want to create the new sub-folder and Project. (Figure 72)



3. Enter a sub-folder name in the Create Subfolder window (Figure 73), then click **Create**.



Note: The name of the location folder is entered automatically in the New Project text box. Ignore this if you do not want to use the same name for folder and project.

Figure 73	Entering name of new sub-folder
Create New 1	Designet [2]
Create New 1	
Select where	you would like the project to go by clicking on the tree view on the left.
Create	new project Dr Moriarty Lab in the 'C:\Command_Console\Data\Dr Moriarty Lab' folder
Create	subfolder Schizophrenia in the 'C:\Command_Console\Data\Dr Moriarty Lab' folder

The new sub-folder appears in the Folders list (Figure 74).

Figure 74 New sub-folder created
Folders
□-1 C:\Command_Console\Data
🖶 🔚 Build37EU133a [Build37EU133a]
🖶 🔚 Default [Default]
📴 🔚 Dr Moriarty Lab [Dr Moriarty]
🖶 🛅 Cancer [Cancer 2, Dr Moriarty]
🗄 🛅 Schizophrenia
🖶 🦳 Dr Smith Lab [Dr Smith]
🖶 🦳 Dr Watson Lab [Data]
🖶 🛅 GCOS 1.3 [GCOS 1.3]
🖶 🛅 Group
h-F-Plus2 [Plus2]

4. Select the folder that you created in the previous steps in the Folder list. The folder name appears in the New Project box and the path to the folder appears. (Figure 75)

Figure 75 Project name entered	
Create New Project 🖻	
Select where you would like the project to go by clic	king on the tree view on the left.
Create new project Schizophrenia	in the 'C:\Command_Console\Data\Dr Moriarty Lab\Schizophrenia' folder

Enter a new project name, if desired, and click Create.
 The selected sub-folder has a project label assigned to it. (Figure 76)



You can also assign a project label to a previously created sub-folder by:

- 1. Selecting the sub-folder in the Folders list
- 2. Entering a Project name in the New Project box and clicking the **Create New Project** button.

Managing existing projects

The Manage Existing Projects controls of the Manage Projects page (Figure 77) enables you to:

- Add an existing sub-folder to a previously created project.
- Specify a Primary sub-folder for a project with multiple sub-folders. A Primary sub-folder functions as the default folder for the project. The Primary sub-folder cannot be deleted.
- Delete sub-folders that are not Primary sub-folders.
- Delete a selected Project.

Note: This deletes only the Project label. The sub-folders and files are not deleted.

4



Figure 77 Manage Existing P	rojects controls		
Manage existing projects 😫			
Select Project: Schizophrenia	the project name only. The	data and folders are n	10t deleted.
Root folders in the "Schizophrenia" proj	ect		
Select the folder you would like to add to t	he project by clicking on th	e tree view on the left	,
Folder	Primary Delete		
C:\Command_Console\Data\Dr Watson Lab\Schizophrenia	×		

Adding an existing sub-folder to a previously created project

- 1. Select the project from the Select Project drop-down list (Figure 77).
- 2. Select the sub-folder to be added in the Folders list.

Note: You can assign a sub-folder to more than one project.

The Add button appears with the path of the selected folder (Figure 78).

Figure 78 Add button with pa	th	
Manage existing projects 🖾		
Select Project: Schizophrenia		
Delete project name. This deletes t	he project name only. T	he data and folders are not deleted.
Root folders in the 'Schizophrenia' proje	ect Data\Dr Smith Lab\Me	antal Illness' folder to the 'Schizophrenia' project
Ci\Command Console\Data\Dr Watson		
Lab\Schizophrenia		
C:\Command_Console\Data\Dr Moriarty Lab\Schizophrenia	— ×	

3. Click Add.

Ŀ

The selected sub-folder is added to the Projects Folder list (Figure 79).



Figure 79 Folder added to Projects Folder list

Root folders in the 'Schizophrenia' project

Select the folder you would like to add to the project by clicking on the tree view on the left.

Folder	Primary	Delete
C:\Command_Console\Data\Dr Watson Lab\Schizophrenia		×
C:\Command_Console\Data\Dr Moriarty Lab\Schizophrenia		×
C:\Command_Console\Data\Dr Smith Lab\Mental Illness		×

Projects with multiple folders will have one folder specified as the primary folder. When files are assigned to the project during registration, they are placed in the Primary folder for the project. The Primary folder cannot be removed from the project; you must designate another folder as the Primary or delete the entire project.

Designating a primary sub-folder for a project

- Select the project from the Select Project drop-down. The folders associated with the project are displayed in the Project Folder list (Figure 79).
- 2. For the folder you want to designate as primary, click the Primary check box. The folder is designated as the primary folder.

Removing sub-folders from a project

1. Select the project from the Select Project drop-down.

The folders associated with the project are displayed in the Project Folder list (Figure 79).

2. Click the red X for the folder you want to remove.

The sub-folder is removed from the project.

Note: You cannot remove primary folders from the project using this method. Designate another folder as primary or delete the entire project, as described above.

Deleting a project

1. Select the project from the Select Project drop-down.

The folders associated with the project are displayed in the Project Folder list (Figure 79).

2. Click the Delete Project Name button.

The project is deleted.

Note: This deletes only the Project label. The sub-folders and files are not deleted.



Generating reports and summaries

You can generate:

- Reports for selected Sample Files.
- A summary report file for the Sample files in a Project.

Generating reports for selected sample files

You can generate a report file in a tab-delimited text format on selected Sample (ARR) files, which you can then view in a text editor or spreadsheet program.

You can also create a Batch Edit file for the selected sample (ARR) file. See "Creating the batch edit file" on page 145 for more information.

Generating a report for selected Sample files

- 1. Select the Sample files from the:
 - Folder view page
 - Project view page
 - Search Results page
- 2. From the Command to Select drop-down (Figure 80), select **Create Report from Selected Arr files** link.

Figure 80 Create Report command							
Command to Run <select a="" command=""></select>							
<select a="" command=""> Copy Selected Files</select>				<select a="" command=""> Copy Selected Files</select>			
:ode	<u>Pos</u>	<u>Probe</u> Array Type	<u>Date M</u>	Create Report From Selected ARR Files Create Batch Edit File From Selected ARR Files Change Probe Array Type			
					-		

The report is created and the Summary page opens (Figure 81).

Figure 81 Summary page	
Search Files By: 🛛 Array Name 🕑	٩
HOME DATA SAMPLES ADMINISTRATION HELP	
Generate Summary of Sample Files 🛙	
Report file ' <desktop>\Downloads\Report_5.rpt' was created successfully.</desktop>	

The page displays the location and file name of the report.

The report file can be viewed in a text editor or spreadsheet program.

Generating a project summary

The report can be used to review data.

Generating a Project Summary

1. From the Administration menu, select $Projects \rightarrow Summary$. The Generate Summary page opens.

You can create a report for the Sample (ARR) files in a project.

- 2. Select the project you want a report on from the drop-down list.
- 3. Click the **Create** button.

The Summary page displays the name and location of the generated report. The report file can be viewed in a text editor or spreadsheet program.

Copying files

The Copy Files function enables you to select files and place a copy of those files to a new location. You can select:

- The Sample (ARR) files in a project.
- Selected Sample (ARR) files in:
 - Folder view page
 - Project view page
 - Search Results page

This can be useful for giving other users access to data.

Projects are described in "Using projects to organize data" on page 78 of this manual.

Note: You can copy to any folder you have access to, as you are not limited to copying files only to a Data Root or sub-folder.

Copying files associated with a project

1. From the Data menu, select **Copy Project**.

The Copy files page opens. (Figure 82)



Figure 82 Copy Files pa	ge
	Search Files By: Anay Name 🗸 (use * for wildcard suffix) 🔤 Advanced Search
HOME DATA SAMPLES A	MINISTRATION HELP
Copy Files	
Copy Files allows you to place a copy of the This can be useful for giving other users acce: • Sample (ARR) • Audit • Image (DAT) • Intensity Data (CEL) • Probe level summarization (CHP)	files associated with a project to a new location. is to data. You can select different file types for copying.
Folders	Destination C:\Command_Console\More_Data (Example C.\Temp)
Archive_calvin_Docs_03_16 Group Group Calvin_Configurations Group Calvin_Docs Group Calvin_W6	Select the project that you want to copy. COOS 1.3 V Include these file types Sample (ARR) files Audit (AUDIT) files V Incarge (DAT) files
erricons Command_Console	✓ Intensity Data (CEL) files ☐ Probe Level Summanization (CHP) files
e - Datax - Datax - Datax - Datax	Сору
- Library	Status from current or last attempted copy. Status From To
HrLogs	Copy Complete Complete
H- New_Root	Copy Complete C.\Command_Console\Data\Build37EU133a\Build37EU133a.CEL C.\Command_Console\Data\New_Project3 Build37EU133a.CEL
⊕-⊡SimData ⊕-⊡Templates	Copy Complete C.\Command_Console\Data\Build37EU133a\Build37EU133a.DAT Build37EU133a.DAT
DEC_Test_Files Decuments and Settings	

2. Select a destination folder from the Folders List, or

Enter the path to the destination folder in the Destinations box.

- 3. Select a project for copying from the Projects drop-down.
- 4. Select the file types you want to copy:
 - Sample (ARR)
 - Audit
 - Image (DAT)
 - Intensity Data (CEL)
 - Probe level summarization (CHP)
 - The file types are described in "File types" on page 56.
- 5. Click Copy.

The progress of the transfer is displayed in the Status window.



Figure	83 Status window						
Status from	Status from current or last attempted copy.						
Status	From	То					
Copy Complete	C:\Command_Console\Data\GCOS 1.3\abcde.ARR	H:\Command_Console\Data\New_Project\abcde.ARR					
Copy Complete	C:\Command_Console\Data\GCOS 1.3\fghij.ARR	H:\Command_Console\Data\New_Project\fghij.ARR					
Copy Complete	C:\Command_Console\Data\GCOS 1.3\GCOS 1.3.ARR	H:\Command_Console\Data\New_Project\GCOS 1.3.ARR					
Copy Complete	C:\Command_Console\Data\GCOS 1.3\GCOS 1.3.CEL	H:\Command_Console\Data\New_Project\GCOS 1.3.CEL					
Copy Complete	C:\Command_Console\Data\GCOS 1.3\klmin.ARR	H:\Command_Console\Data\New_Project\klmin.ARR					
Copy Complete	C:\Command_Console\Data\GCOS 1.3 \New_Sample_File.ARR	H:\Command_Console\Data\New_Project\New_Sample_File.ARR					
Copy Complete	C:\Command_Console\Data\GCOS 1.3\opqrst.ARR	H:\Command_Console\Data\New_Project\opqrst.ARR					
Copy Complete	C:\Command_Console\Data\GCOS 1.3\Sample1.ARR	H:\Command_Console\Data\New_Project\Sample1.ARR					
Copy Complete	C:\Command_Console\Data\GCOS 1.3\Sample4.ARR	H:\Command_Console\Data\New_Project\Sample4.ARR					

Copying selected files

- 1. Select the Sample files from the:
 - Folder view page
 - Project view page
 - Search Results page
- 2. From the Command to Select drop-down, select **Create Report from Arr files** in List link.

The Copy files page opens (Figure 84).



Figure 84 Copy Files	page			
HOME DATA SAMPLES AD	INISTRATION	HELP ·		
Copy Files Copy Files allows you to place a copy of the fil This can be useful for giving other users access • Sample (ARR) • Audt • Image (DAT) • Intensity Data (CEL) • Probe level summarization (CHP)	es associated with a projec to data. You can select diff	t to a new location. Terent file types for copying:		
Taldare				
E- S Ci\	Destination		(Example C:\Temp)
CMCommand_ConsoleUatalNew_Project3Build37EU133a.ARR CNCommand_ConsoleUatalNewJPr0133alFuild37EU133a.ARR CNCommand_ConsoleUatalNew_Project3Build37EU133a.CEL CNCommand_ConsoleUatalNew_Project3Build37EU133a.CHP CNCommand_ConsoleUatalNew_Project3Build37EU133a.DAT CNCommand_ConsoleUatalNewJ7EU133alFuild37EU133a_DAT CNCommand_ConsoleUatalNewJ7EU133alFuild37EU133a_AbBrobeMarkScaing CHP CNCommand_ConsoleUatalNewJ7EU133alFuild37EU133a_AbBrobeMarkScaing CHP CNCommand_ConsoleUatalNewJ7EU133alFuild37EU133a_AbBrobeMarkScaing CHP CNCommand_ConsoleUatalNewJ7EU133alFuild37EU133a_AbBrobeMarkScaing CHP CNCommand_ConsoleUatalNewJ7EU133alFuild37EU133a_ComProbeMarkScAing CHP CNCommand_ConsoleUatalNewJ7EU133alFuild37EU133a_ComProbeMarkCHP CNCommand_ConsoleUatalNewJ7EU133alFuild37EU133a_ComProbeMarkCHP CNCommand_ConsoleUatalNewJ7EU133alFuild37EU133a_comProbeMark CHP CNCommand_ConsoleUatalNewJ7EU133alFuild37EU133a_comProbeMark CHP CNCommand_ConsoleUatalNewJ7EU133alFuild37EU133a_comProbeMark CHP CNCommand_ConsoleUatalNewJ37EU133alFuild37EU133a_comProbeMark CHP CNCommand_ConsoleUatalNewJ37EU133alFuild37EU133a_comProbeMark CHP CNCommand_ConsoleUatalNewJ37EU133alFuild37EU133a_comProbeMark CHP CNCommand_ConsoleUatalNewJ37EU133alFuild37EU133a_comProbeMark CHP CNCommand_ConsoleUatalNewJ37EU133alFuild37EU133a_comProbeMark CHP CNCommand_ConsoleUatalNewJ37EU133alFuild37EU133a_comProbeMark CHP CNCommand_ConsoleUatalNewJ37EU133alFuild37EU133a_comProbeMark CHP CNCommand_ConsoleUatalNewJ37EU133alFuild37EU133alFuild37EU133a_comProbeMark CHP CNCommand_ConsoleUatalNewJ37EU133alFuild37EU133alFuild37EU133a_comProbeMark CHP CNCommand_ConsoleUatalNewJ37EU133alFuild37EU133alFuilf3a_comProbeMark CHP CNCommand_ConsoleUatalNewJ37EU133alFuild37EU133alFuilf5a_comProbeMark CHP CNCommand_ConsoleUatalNewJ37EU153alFuilf5a_comProbeMark CHP CNCommand_ConsoleUatalNewJ57EU153alFuilf5a_comProbeMark CHP CNCommand_ConsoleUatalNewJ57EU153alFuilf5a_comProbeMark CHP CNCommand_ConsoleUatalNewJ57EU153alFuilf5a_comProbeMark CHP CNCOmmand_ConsoleUa				kScaling CHP eMask CHP beMask CHP T
	Status	From		To
	Copy Complete	C:\Command_Console\Data\GC	OS 1.3\abcde.ARR	H:\Command_Console\Data\New_Project\abcde.ARR
	Copy Complete	C:\Command_Console\Data\GC	OS 1.3\fghij.ARR	H:\Command_Console\Data\New_Project\fghij.ARR
	Copy Complete	C:\Command_Console\Data\GC	OS 1.3\GCOS 1.3.ARR	H:\Command_Console\Data\New_Project\GCOS 1.3.ARR
	Copy	ava	0.01.2000.01.2.0ET	TUG

3. Select a destination folder from the Folders List, or

Enter the path to the destination folder in the Destinations box.

- 4. Review the Files to be copied list.
- 5. Click Copy.

The progress of the transfer is displayed in the Status window (Figure 85).

Figure 85 Status window					
Status from	. current or last attempted copy.				
Status	From	To			
Copy Complete	C:\Command_Console\Data\GCOS 1.3\abcde.ARR	H:\Command_Console\Data\New_Project\abcde.ARR			
Copy Complete	C:\Command_Console\Data\GCOS 1.3\fghij.ARR	H:\Command_Console\Data\New_Project\fghij.ARR			
Copy Complete	C:\Command_Console\Data\GCOS 1.3\GCOS 1.3.ARR	H:\Command_Console\Data\New_Project\GCOS 1.3.ARR			
Copy Complete	C:\Command_Console\Data\GCOS 1.3\GCOS 1.3.CEL	H:\Command_Console\Data\New_Project\GCOS 1.3.CEL			
Copy Complete	C:\Command_Console\Data\GCOS 1.3\klmin.ARR	H:\Command_Console\Data\New_Project\klmin.ARR			
Copy Complete	C:\Command_Console\Data\GCOS 1.3 \New_Sample_File.ARR	H\Command_Console\Data\New_Project\New_Sample_File ARR			
Copy Complete	C:\Command_Console\Data\GCOS 1.3\opqrst.ARR	H:\Command_Console\Data\New_Project\opqrst.ARR			
Copy Complete	C:\Command_Console\Data\GCOS 1.3\Sample1.ARR	H:\Command_Console\Data\New_Project\Sample1.ARR			
Copy Complete	C.\Command_Console\Data\GCOS 1.3\Sample4.ARR	H'\Command_Console\Data\New_Project\Sample4.ARR			



Specifying a default folder

The Default folder is used as a destination folder for data when:

- Performing Drop and Scan.
- Scanning data for an array for a Sample (ARR) file located on another computer, connected through a network.

See Appendix A, "Networking" on page 338 for more information on the Network functionality of GCC.

When GCC is installed, C:\Command_Console\Data\Default is used for the default folder.

You can change the Default folder if you want.

Changing the Default folder

1. From the Data menu, select **Default Folder**.

The Set Default Folder page appears. (Figure 86)

Figure 86 Set Default Fo	lder		
	Search Files By: 🛛 Array Name 💌	(use * for wildcard suffix)	Advanced Search
HOME DATA SAMPLES ADMI	NISTRATION HELP		
Set Default Folder			
The Default folder is used for scan data when: • Performing Drop and Scan • Scanning data or an array for a Sample (.ARR) Select new default folder from the folder birt. • Colormand_ConsoleNota • Colormand_ConsoleNota • Colormand_ConsoleNter_Root	file located on another computer, connected through a network. Current Default Folder: CACommand_Console/Data	a	

A Folder list is displayed on the left side of the page. The right side displays the current default folder and the selection controls.

- 2. Select a folder from the Folder list. You can select a data root or a sub-folder.
- 3. Click Set.

The selected folder is used for the Default folder.



Uploading data to network data storage

You can create Sample (ARR) files on any data root your GCC system has access to, including network data storage. However, you cannot create DAT files over a network connection to network data storage; instead, the DAT files are created in the Default folder on the local computer. This is done to protect the DAT file from any problems related to the networks, so that an array can always be scanned successfully even when a network is unreliable.

The Upload Data function can be used to automatically transfer DAT, CEL, and other files from the Default folder to the network data storage where the Sample (ARR) file is located. Upload Data is useful when you want to consolidate data from different workstation computers onto one network data storage site.

The use of the Data Upload function is explained in:

- "Uploading data manually" on page 94
- "Scheduling auto-uploads" on page 96

The Overview section below provides information on why you may want to use the Upload Data function.

Overview You can create Sample (ARR) files on any data root your GCC system has access to, including network data storage.

However, you cannot create DAT files over a network connection to network data storage; instead, the DAT files are created in the Default folder on the Scanner Workstation computer (Figure 87). This is done to protect the DAT file from any problems related to the networks, so that an array can always be scanned successfully even when a network is unreliable.



The Upload Data function can be used to automatically transfer DAT and CEL files from the Default folder to the network data storage where the Sample (ARR) file is located (Figure 88). Upload Data is useful when you want to consolidate data from different workstation computers onto one network data storage site.





Uploading data manually

1. From the Data menu, select **Upload Data.**

The Upload Data page is displayed. (Figure 89)

Figure 89 Upload Data page	
Search Files By: 🛛 Array Name 🔽 (Use * for wildcard) 🗖 Advanced Search	٩
HOME DATA SAMPLES ADMINISTRATION HELP	_
Upload Data 🖻	
Upload Data moves DAT, CEL, CHP and JPG files in the default folder or any subfolder of the default folder to the same location where the sample (.ARR) file is located. When a sample file is on a network share (example \\server\path\) the DAT, CEL, JPG and optionally CHP files will be created locally in the default folder.	

A new window opens with info on the files to be uploaded. (Figure 90)

	Search Files By: 🖾 Array Name 🛛 🛛		(Use * for wildcard) 🔤 Advanced Se	earch 🔅
НОМЕ	DATA SAMPLES ADMINISTRATION HELP			
Uple	oad Data 🛙			
Uploa the sa CHP f File 12 Fil	ad Data moves DAT, CEL, CHP and JPG files in the ample (.ARR) file is located. When a sample file iiles will be created locally in the default folder. s to upload Select All Unselect All Start Upload les available for upload. 12 Selected. Sorted by	ne default folder or any subfolo : is on a network share (examp 'From' Ascending	er of the default folder to the same loca le \\server\path\) the DAT, CEL, JPG and	ation where d optionally
Select	From	To	Status	
	C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).CEL	\\shares\SantaClara\Personal\rallso\AGCC_I	Data\Other_Data Not Started	
	C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).DAT	\\shares\SantaClara\Personal\rallso\AGCC_I	Pata\Other_Data Not Started	
	C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).JPG	\\shares\SantaClara\Personal\rallso\AGCC_I	Data\Other_Data Not Started	
	C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).CEL	\\shares\SantaClara\Personal\rallso\AGCC_I	Data\Other_Data Not Started	
	C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DAT	\\shares\SantaClara\Personal\rallso\AGCC_I	Data\Other_Data Not Started	
	C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).JPG	\\shares\SantaClara\Personal\rallso\AGCC_I	Data\Other_Data Not Started	
	C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2)_2.CEL	\\shares\SantaClara\Personal\rallso\AGCC_I	ata\Other_Data Not Started	
	C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2)_2.DAT	\\shares\SantaClara\Personal\rallso\AGCC_I	Data\Other_Data Not Started	
	C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2)_2.JPG	\\shares\SantaClara\Personal\rallso\AGCC_I	Data\Other_Data Not Started	
	C:\Command_Console\Data\Default\Sample_14_(HG-U133A_2).CEL	\\shares\SantaClara\Personal\rallso\AGCC_I	ata\Other_Data Not Started	
	C:\Command_Console\Data\Default\Sample_14_(HG-U133A_2).DAT	\\shares\SantaClara\Personal\rallso\AGCC_I	ata\Other_Data Not Started	
	C:\Command_Console\Data\Default\Sample_14_(HG-U133A_2).JPG	\\shares\SantaClara\Personal\rallso\AGCC_I	Data\Other_Data Not Started	

The page displays a list of data files in the Default folder that are associated with a Sample (ARR) file on a network drive:

From	Current location and file name.
То	The file destination (location of the Sample (ARR) file).
Status	The current status of the move.

2. Click **Start Uploading** to upload the files to the locations.

A notice informs you that the move is in progress. (Figure 91)

		
Search Files By: 😰 Array Name	✓ (Use * for wildcard)	Ivanced Search
HOME DATA SAMPLES ADMINISTRATION H	IELP	
Upload Data 🛙		
Upload Data moves DAT, CEL, CHP and JPG file the sample (.ARR) file is located. When a sam CHP files will be created locally in the default f Files to upload Select All Unselect All Start U Upload is Running. 4 of 12 successfully upload	es in the default folder or any subfolder of the default folder to the ple file is on a network share (example \\server\path\) the DAT, Clear of the default folder of the plant of the default folder.	e same location where EL, JPG and optionally
Uploading file 5 of 12 💥 Stop		
Uploading file 5 of 12 🗱 Stop	То	Status
Uploading file 5 of 12 🗱 Stop From C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).CEL	Io \\shares\SantaClara\Personal\vallso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).CEL	Status Upload Complete
Uploading file 5 of 12 🔅 Stop From C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).CEL C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).DAT	To \\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).CEL \\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).DAT	Status Upload Complete Upload Complete
Uploading file 5 of 12 🗱 Stop From C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).CEL C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).DAT C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).JRG	Io \\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).CEL \\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).DAT \\shares\SantaClaraPersonal\rallso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).JPG	Status Upload Complete Upload Complete Upload Complete
Uploading file 5 of 12 🗱 Stop From C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).CEL C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).PG C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).PG C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).CEL	Io \\shares\SantaClara\Personal\vallso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).CEL \\shares\SantaClara\Personal\vallso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).DAT \\shares\SantaClara\Personal\vallso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).2GL \\shares\SantaClara\Samplavallso\AGCC_Data\Other_Data\Sample_12_(HG-U133A_2).CEL	Status Upload Complete Upload Complete Upload Complete
Uploading file 5 of 12 ** Stop From C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).CEL C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).DAT C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).GEL C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).CEL C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).CEL	To \\shares\SantaClare\Personal\rallso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).CEL \\shares\SantaClare\Personal\rallso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).DAT \\shares\SantaClare\Personal\rallso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).JPG \\shares\SantaClare\Personal\rallso\AGCC_Data\Other_Data\Sample_12_(HG-U133A_2).CEL T\\shares\SantaClare\Personal\rallso\AGCC_Data\Other_Data\Sample_12_(HG-U133A_2).CEL T\\shares\SantaClare\Personal\rallso\AGCC_Data\Other_Data\Sample_12_(HG-U133A_2).CEL	Status Upload Complete Upload Complete Upload Complete DAT In progress
Uploading file 5 of 12 ** Stop From C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).CEL C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).DAT C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DET C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).CEL C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DET C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DET C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DET	IO \\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).CEL \\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).DE \\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data\Sample_12_(HG-U133A_2).DE \\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data\Sample_12_(HG-U133A_2).DE \\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data\Sample_12_(HG-U133A_2).CEL AT \\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data\Sample_12_(HG-U133A_2).CL \\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data\Sample_12_(HG-U133A_2).CL	Status Upload Complete Upload Complete Upload Complete DAT In progress Not Started
Uploading file 5 of 12 ** Stop From C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).CEL C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).DF C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DF C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).CEL C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DF C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DF C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DF	Io \\shares\SantaClara\Personal\vallso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).CEL \\shares\SantaClara\Personal\vallso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).DAT \\shares\SantaClara\Personal\vallso\AGCC_Data\Other_Data\Sample_12_(HG-U133A_2).JGL \\shares\SantaClara\Personal\vallso\AGCC_Data\Other_Data\Sample_12_(HG-U133A_2).CEL T\\shares\SantaClara\Personal\vallso\AGCC_Data\Other_Data \\shares\SantaClara\Personal\vallso\AGCC_Data\Other_Data \\shares\SantaClara\Personal\vallso\AGCC_Data\Other_Data \\shares\SantaClara\Personal\vallso\AGCC_Data\Other_Data	Status Upload Complete Upload Complete Upload Complete DAT In progress Not Started Not Started
Uploading file 5 of 12 ** Stop From C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).CEL C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).DAT C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DGT C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).CEL C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).CEL C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).2CEL C:\Command_CONSOLE\Data\Default\Sample_12_(HG-U133A_2).2CEL C:\Command_CONSOLE\Data\Default\Sample_12_(HG-U133A_2).2CEL C:\Command_CONSOLE\Data\Default\Sample_12_(HG-U133A_2).2CEL C:\Command_CONSOLE\Data\Default\Sample_12_(HG-U133A_2).2CEL C:\Command_CONSOLE\Data\Default\Sample_12_(HG-U133A_2).2CEL C:\Command_CONSOLE\Data\Def	Io \\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).CEL \\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).DAT \\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).3PG \\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data\Sample_12_(HG-U133A_2).2L AT \\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data Sample_12_(HG-U133A_2).2L \\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data Sample_12_(HG-U133A_2).2L \\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data Sample_12_(HG-U133A_2).2L \\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data	Status Upload Complete Upload Complete Upload Complete DATIn progress Not Started Not Started Not Started
Uploading file 5 of 12 ** Stop From C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).CEL C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).DAT C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DET C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DET C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DET C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DET C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DET C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DET C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DET C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).2.DF	Io (\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).CEL (\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).DEL (\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data\Sample_12_(HG-U133A_2).DEG (\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data\Sample_12_(HG-U133A_2).CEL T\\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data\Sample_12_(HG-U133A_2).CEL (\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data Sample_12_(HG-U133A_2).CEL (\shares\SantaClara\Personal\rallso\AGCC_Data\Other_Data	Status Upload Complete Upload Complete Upload Complete Upload Complete Not Started Not Started Not Started Not Started
Uploading file 5 of 12 ** Stop From C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).CEL C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).DE C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).DE C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DE C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DE C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DE C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DE C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DE C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DE C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).2CE C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).2D C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).CEL	Io \\shares\SantaClara\Personal\raliso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).CEL \\shares\SantaClara\Personal\raliso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).DAT \\shares\SantaClara\Personal\raliso\AGCC_Data\Other_Data\Sample_12_(HG-U133A_2).DGT \\shares\SantaClara\Personal\raliso\AGCC_Data\Other_Data\Sample_12_(HG-U133A_2).DGT \\shares\SantaClara\Personal\raliso\AGCC_Data\Other_Data\Sample_12_(HG-U133A_2).DGT \\shares\SantaClara\Personal\raliso\AGCC_Data\Other_Data \\shares\SantaClara\Personal\sinal\Sonal\SCC_Data\Other_Data \\shares\SantaClara\Personal\sinal\Sonal\SCC_Data\Other_Data \\shares\SantaClara\Personal\sinal\Sonal\SCC_Data\Other_Data \\shares\SantaClara\Personal\sinal\Sonal\SCC_Data\Other_Data \\shares\SantaClara\Personal\SantaClara\Personal\Sonal\SCC_Data\Other_Data \\shares\SantaClara\Personal\Sonal\Sonal\SCC_Data\Other_Data \\shares\SantaClara\Personal\Sonal\Sonal\Sonal\SCC_Data\SCC_Data\Other_Data \\shares\San	Status Upload Complete Upload Complete Upload Complete Upload Complete DAT In progress Not Started Not Started Not Started Not Started Not Started
Uploading file 5 of 12 ** Stop From C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).CEL C:\Command_Console\Data\Default\Sample_11_(HG-U133A_2).DAT C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DGT C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).CEL C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).CEL C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DCE C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DCE C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DCE C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DCE C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DCE C:\Command_Console\Data\Default\Sample_12_(HG-U133A_2).DAT C:\Command_Console\Data\Default\Sample_14_(HG-U133A_2)	Io Vahres\SantaClars\Personal\vallso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).CEL Vahres\SantaClars\Personal\vallso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).DAT Vahres\SantaClars\Personal\vallso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).DAT Vahres\SantaClars\Personal\vallso\AGCC_Data\Other_Data\Sample_11_(HG-U133A_2).DEL Vahres\SantaClars\Personal\vallso\AGCC_Data\Other_Data\Sample_12_(HG-U133A_2).CEL Vahres\SantaClars\Personal\vallso\AGCC_Data\Other_Data Sample_12_(HG-U133A_2).CEL Vahres\SantaClars\Personal\vallso\AGCC_Data\Other_Data	Status Upload Complete Upload Complete Upload Complete Upload Complete DAT In progress Not Started Not Started Not Started Not Started Not Started Not Started

The status of the move is displayed in the lower part of the page, with a list of the files that have been transferred and their status.

When the upload is finished, the status is displayed in the page. (Figure 91)

The uploaded files can be seen in their new location. (Figure 92)

Figure 92 Data in new	locat	ion										
Search File	Search Files By: 🛙 Array Name 🔽 (Use * for wildcard) 🗖 Advanced Search 🤑 🎒							۹				
HOME DATA SAMPLES ADMINISTRATION HELP												
Folders	Curre	nt Folder: \\shares\Santa	Clara\Pe	rsonal\ra	llso\GCC	_Data\Oth	er_Data S	orted I	by 'File N	ame'		
	Open	Add Subfolder Renai	ne									
Other_Data [Other_Data]	View	Default 👻 Customize	File	filter Sho	w	 Custom 	ize					
C:\Command_Console\Data	12 File	s, 0 Selected Select All	Unsel	ect All	Commai	nd to Run	<select a="" con<="" td=""><td>nmand></td><td></td><td></td><td>¥</td><td></td></select>	nmand>			¥	
Checked_SNPs Checked_SNPs Checked_SNPs	Selected	File Name	<u>Project</u> <u>Name</u>	Array Name	<u>Barcode</u>			<u>Lot</u> Numbe	Expiration Tr Date	Probe Array Type	Date Modified	A
B- Dr Moriarty [Dr Moriarty]												
+ Drop_n_Scan [Drop_n_Scan]		Sample 11.ARR	Other_Dat	Sample_11 a (HG- U133A_2)		0461817101308	401416533711	4014165	5 10/13/2008	HG- U133A_3	2 8/4/2008 10:36:25	АМ
BrForDanny_2 BrMitoV2		Sample 11 (HG-U133A 2).CEL	Other_Dat	Sample_11 a (HG- U133A_2)		0461817101308	401416533711	4014165	5 10/13/2008	HG- U133A_	2 8/4/2008 10:36:51	АМ
Reconnect_CEL_CHP [Reconnect_CEL_CHP]		Sample 11 (HG-U133A 2).DAT	Other_Dat	Sample_11 a (HG- U133A 2)	@5200650	0461817101308	401416533711	4014165	5 10/13/2008	HG- U133A_3	2 8/4/2008 10:36:35	АМ
B- Reconnect_DAT_CEL [Reconnect_DAT_CEL] B- ReSeq [ReSeq]		Sample 12.ARR	Other_Dat	Sample_12 a (HG- U133A_2)	@5200650	0461817101308	401416533712	4014165	5 10/13/2008	HG- U133A_3	2 8/4/2008 10:40:47	АМ
B- Reseq_02 B- Reseq_03		Sample 12 (HG-U133A 2).CEL	Other_Dat	Sample_12 a (HG- U133A_2)	@5200650	0461817101308	401416533712	4014165	5 10/13/2008	HG- U133A_	2 8/4/2008 10:38:59	АМ
Restore_Drop_and_Scan [Restore_Drop_and SNP6_Data		Sample 12 (HG-U133A 2).DAT	Other_Dat	Sample_12 a (HG- U133A_2)	@5200650	0461817101308	401416533712	4014165	5 10/13/2008	HG- U133A_3	2 8/4/2008 10:38:46	АМ
B- Universal		Sample 12 (HG-U133A 2) 2.CE	Other_Dat	Sample_12 a (HG- U133A_2)	@5200650	0461817101308	401416533712	401416	5 10/13/2008	HG- U133A_3	2 8/4/2008 10:41:13	АМ
		Sample 12 (HG-U133A 2) 2.DA	T Other_Dat	Sample_12 a (HG- U133A_2) Sample_13	@5200650	0461817101308	401416533712	4014165	5 10/13/2008	HG- U133A_3	2 8/4/2008 10:40:58	АМ





Scheduling autouploads

The Data Uploader Scheduler enables you to run the Data Upload automatically on a schedule you determine.

1. Click the **Data Uploader** icon 算 in the Launcher.

The GCC Data Uploader Scheduler window opens. (Figure 93)

Figure 93 GCC Data Uploader Scheduler, Task tab.
Task Schedule Settings
C:\WINDOWS\Tasks\GCC Data Uploader.job
Run: Command Console\Uploader.exe
Browse
Start in:
Comments:
Run as: NT AUTHORITY\SYSTEM Set password
☐ Run only if logged on ✓ Enabled (scheduled task runs at specified time)
OK Cancel

The dialog box has three tabs:

- Task
- Schedule
- Settings

The Task tab enables you to set the options for the task itself.

2. In the **Run** box, enter the path to the file to be run as a scheduled task.

Use quotation marks around the task path if the path includes spaces.

- 3. Enter information in the Start In box on the location of the folder with the task or other necessary files.
- 4. Use the Comments box for notes about the task.
- In the Run As box, enter the user account for running the scheduled task. Specify user account (must be the same account used for the GCC Services, with
- permissions on both the computer and the remote storage location).
- 6. Enter the password for the user account:
 - a. Click Set Password.

The Set Password dialog box opens (Figure 94).



Figure 94	Set Password dialog box
Password:	
Confirm password:	
	DK Cancel

- b. Enter and confirm the password for the user account and click **OK** in the Set Password dialog box.
- 7. Select other options:
 - Run only if logged on.
 - Enabled (scheduled task runs at specified time).
- 8. Click the **Schedule** tab to set up the schedule for the upload.

The default setting is to run the upload function daily at 2 AM.

Figure 95 Schedule tab with settings for daily task
Task Schedule Settings At 2:00 AM every day, starting 8/1/2008 Schedule Task: Start time: Daily 2:00 AM Advanced
Schedule Task Daily <u>Every</u> 1 <u>;</u> day(s)
OK Cancel

The Schedule tab (Figure 95) provides options for setting the schedule.

- 9. Select a period for performing the task from the Schedule Task drop-down. You can schedule the task to run:
 - Daily
 - Weekly
 - Monthly
 - Once
 - At System Startup
 - At Logon

• When idle

The options for task schedule change with the time period (Figure 96).

Figure 96	Settings f	or Wee	ekly task	
<u>S</u> chedule Task:	Start time:		,	
Weekly	1:01 PM	•	Ad <u>v</u> anced	
Schedule Task Wee	ekly	=	E a .	
	week(s) on:	IV Mon ∏ Tue	∣ Sat ∏ Sun	
		∏ Wed		
		Fri Fri		

Click **Advanced Options** (Figure 97) to set Start/Stop dates and to specify how often to repeat the task.

10. Enter a time for the task to start in the Start time box.

Figure 97 Advanced Schedule (dialog box	Options
Start Date: Friday , August 01	, 2008 💌
OK _	Cancel

- 11. You can enter multiple schedules:
 - a. Select the Show Multiple Schedules check box.

A schedule drop-down list appears at the top of the tab screen with **New** and **Delete** buttons.

Figure 98 Multiple schedules
Task Schedule Settings
2. At 3:00 AM every day, starting 8/15/2008
<u>N</u> ew <u>D</u> elete
<u>S</u> chedule Task: Start time: Daily ♥ 9:00 AM ★ Advanced
Schedule Task Daily Every 1 day(s)
Show multiple schedules.
OK Cancel

- b. Click **New** to create a new schedule.
- c. Set the schedule using the Schedule Task controls, as described in steps 9 and .
- d. Click **Delete** to delete a scheduled task.
- 12. Click the **Settings** tab.

Figure 99 Settings tab
Task Schedule Settings
Scheduled Task Completed
Image: Stop the task if it runs for: 72 ▲ hour(s) 0 ▲ minute(s).
Idle Time
minute(s)
If the computer has not been idle that long, retry for up to:
Stop the task if the computer <u>c</u> eases to be idle.
Power Management
Don't start the task if the computer is running on <u>batteries</u> .
Stop the task if battery mode begins.
☐ Wake the computer to run this task.
OK Cancel

The Settings tab (Figure 99) enables you to set options for the upload:

• Scheduled Task Completed: Use these to set the options for a task that is only running once.



- Idle Time: Use these to start the task only if the computer has been idle for a specified period of time
- Power Management: Use these to set the options for power management if using a laptop.
- 13. Click **OK** when you have finished setting the task, schedule, and settings options.

The task is scheduled and will run at the set times.

When the scheduled time comes, the Upload Utility window (Figure 100) appears on your desktop and shows the progress of the upload.

Figure 100 Upload utility running				
C:\WINDOWS\System32\svchost.exe				
Uploader utility 1.0				
Loading list of files to upload from the folder 'C:\Command_Console\Data\Default '				
12 files available for Upload				
0 of 12 successfully uploaded, 0 warnings, 0 errors. 1 of 12 successfully uploaded, 0 warnings, 0 errors. 4 of 12 successfully uploaded, 0 warnings, 0 errors. 7 of 12 successfully uploaded, 0 warnings, 0 errors. 7 of 12 successfully uploaded, 0 warnings, 0 errors.				

You can set up the GCC Email Configuration Editor to notify you when the Upload Utility runs or if problems arise. See Appendix E, "Notification e-mails" on page 367 for more information.



Creating and editing sample (ARR) files

Sample Registration is the first step in the recommended array processing workflow, as shown in Figure 101.



For information on scanning arrays without registering them first, see "Drop and scan" on page 206.

This chapter describes the following options for creating Sample files and registering arrays:

- "Detailed sample registration" on page 104
- "Quick sample registration" on page 120
- "Batch registration" on page 125
- "Sample prep plate registration" on page 131

"GeneTitan array plate registration" on page 135

You can also edit previously created Sample (ARR) files

- "Editing files and copying attributes" on page 110
- "Adding a barcode to a sample file" on page 142
- "Batch editing" on page 144

For information on selecting a Sample Registration method, see "Registering samples and arrays" on page 25.

See "Introduction to sample registration" for an introduction to the types of information that can be collected in a Sample file.

Introduction to sample registration

To get the most out of GCC, you need to understand the types of information that are collected in the Sample file, as described below:

- "Information in the sample file", below
- "Characters allowed in GCC" on page 104

Information in the sample file

In GCC, the samples are the beginning of the data chain for a given experiment. The sample information is stored in a Sample file with an ARR extension.

The Sample (ARR) file collects two types of information:

- Sample Attributes: information that you can use to interpret the experimental data. It can include information about the sample itself, the experimental conditions, or other information you may find useful.
- Array Information: Information about the array(s) used with the sample. More than one array can be associated with the sample. This might be useful for making sure that data from products that contain more than one array remain related or to help describe experiments that use replicates.

Sample attributes

There are two types of attributes in GCC:

- Template Attributes, which have the attribute name, data type and other information specified in a template.
- For more information on creating and managing templates, see "Working with templates" on page 328.
- User Attributes, which are created individually during registration.

Each attribute in a template is assigned one of the following data types:

- Text: Text string
- Number: Integer or floating point number
- Date: Calendar data
- SingleSelect: Presents a list of items for the user to choose

User Attributes may be Text, Number, or Date data types.

Beta Versions of GCC included other deprecated data types which are no longer available, such as:

- Integer
- Floating Point
- MultiSelect

The data type determines the type of value that can be entered, and the types of comparisons that can be performed during an Advanced Search.

Array information

The Sample file also contains information about the array(s) used with the sample. More than one array can be associated with the sample. This is useful for tracking replicates; in addition, it can be used to simplify tracking data for multi-chip arrays, such as 500K arrays.

Each array is assigned an array name during registration. The array name is used to identify the DAT, CEL, and CHP data files that are generated during analysis. (Figure 102)



The array information includes:

- Array Name
- Probe Array Type
- Barcode

Characters allowed in GCC

You can only use a certain set of characters in GCC Sample File names, Folder Names, Project Names, and Array Names:

These names can contain:

- Basic Latin letters (A-Z, a-z)
- Digits (0-9)
- Spaces
- The following set of punctuation marks: ! # \$ % & '() + , . ; = @ [] ^ _`{} ~
- These names cannot use the following characters: \ / : * ? " <>|

International characters are not allowed.

Sample attribute names can contain:

- Numbers
- Letters
- International characters
- The following set of punctuation marks: ! # % & ' () + , . ; = @ [] ^ \/`~ Sample Attribute names cannot contain any of the following characters: { } : * ? " < > |

Sample attribute values of Text type can contain any characters.

Detailed sample registration

The Detailed Sample Registration page enables you to register a single sample and its associated cartridge arrays, along with any sample attribute you want to include. You can use templates to determine which attributes need to be entered for registration, and you can add user attributes that are unique to that sample.

You cannot register a GeneTitan System array plate using the Detailed Sample Registration (use "GeneTitan array plate registration", described on on page 135).You can add a cartridge array to a previously created array plate Sample file with the editing functions of the Detailed Sample Registration.

For more information see "Creating a new sample file".

The page can also be used for:

- Editing previously created Sample files
- Renaming a Sample file and/or the Array name
- Copying the attribute data over to a new file
- Adding physical arrays to an existing Sample (Arr) file

For more information, see "Editing files and copying attributes" on page 110.

If you have edited or deleted templates and attributes, you may need to change the attributes in a Sample file when you try to edit it. For more information, see "Sample attributes conversion" on page 115.

Creating a new sample file

1. From the Samples menu, select **Register**.

The Detailed Sample Registration page opens (Figure 103).



The Detailed Sample Registration page has four sections:

- Project and File Name (at the top of the page)
- Sample Attributes from Templates
- Additional Sample Attributes
- Arrays list
- 2. Select a Project from the drop-down list (optional) (Figure 104).
- 3. Enter a name in the Sample File Name box (Figure 104).

Figure 104 Entering Project and File Name				
Selected Project: 💷 Dr Moriarty 🗸				
Sample File Name (Required):	Brain_03			

The Sample Attributes from Templates section displays a list of the attributes in the Default template when the page is first opened. See "Managing default templates" on page 335 for more information.

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You can:

- Enter attribute values for the Default template (see Step 6 on page 107).
- Add and remove templates with additional attributes (optional—see Step 4, below).

Figure 105	Sample Attribu	utes from To	emplates	
Add Sample Attrib	outes from Templa	tes (Optional)		
TestA			×	
gender (Require	d): SingleSelect 🔤 👻			
age (Required):	Number			
tissue type:	Text			
	Select 0	ptions		
Select a template which templates to	from the list and cli o use for this sample	ck "Select" to a e.	add attributes from that template to this sam	nple. Click "Options" to change

- 4. To add Templates, use one of the following options:
 - Select the template from the drop-down list and click Select (Figure 106); or

Figure 106	Template List		
Add Sample Attri	ibutes from Templates (Optional))	
TestA		×	
gender (Require	ed): SingleSelect 🔤		
age (Required):	Number		
tissue type:	Text		
MIAME Sample Informat	Select Options the list and click "Select" to for this sample.	add attributes from that template to this sample. C	lick "Options" to change

Click **Options** to open the Template Select page. (Figure 107) **Note:** You can also use the Template Select page to delete templates from the Sample (ARR) file.

Figure 107 Template Select page						
Search Files By: 🔳 🛛	Array Name 🛛 🖌	(Use *	for wildcard) 🧧 Advanced	<u>l Search</u> 🌒		
HOME DATA SAMPLES	ADMINISTRATION HELP					
Templates:	Select Cancel					
Information	Sample Attributes					
🗹 Moriarty	Field Name	Required	Туре	Value		
✓ TestA	Template: TestA					
	gender	Yes	SingleSelect			
	age	Yes	Number			
	tissue type	No	Text			
	Template: Moriarty		arty			
	Patient Height	Yes	Number			
	Patient Weight	Yes	Number			
	Date of Death	No	Date			

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The Template Select page displays a list of the available templates on the left side.

The right side displays a list of the attributes in the selected templates.

- Select the template(s) you want to use.
- Review the attributes in those templates in the Sample Attribute list.
- Click Select to add selected templates to the Sample (ARR) File.

The Detailed Sample Registration page returns with the attributes in the selected template(s) displayed (Figure 108).

Click **Cancel** to return to the Detailed Sample Registration page without adding templates.

Figure 108 Added Templates			
Add Sample Attributes from Templates (C	ptional)		
TestA	×	<	Click to delete
gender (Required): SingleSelect	×		selected template and
age (Required): Number 4			all attributes
tissue type: Text			all attributes
Moriarty	×	-	
Patient Height (Required): Number			
Patient Weight (Required): Number			
Date of Death: Date			
Select Options Select a template from the list and click "Se which templates to use for this sample.	lect" to add attributes from that template to this sample. Cli	ck "Options	" to change

- 5. To delete a selected template and all its attributes, click the red X at the top of the template's attribute list (Figure 108).
- 6. To enter values for the Template Attributes:
 - a. Enter values for the text, numerical, and date attributes.
 - b. Select values from the drop down lists for the SingleSelect attributes (Figure 109).

Figure 109 Entering values for the sample attributes	
Add Sample Attributes from Templates (Optional)	
TestA 🗙	
gender (Required): SingleSelect M • age (Required): Number M tissue type: Text F	
Moriarty X	
Patient Height (Required): Number Patient Weight (Required): Number Date of Death: Date	
Select Options Select a template from the list and click "Select" to add attributes from that template to this sample. Clic which templates to use for this sample.	ck "Options" to change

- 7. Add user-defined attributes to the Sample by using the Additional Sample Attributes list:
 - a. Click Add under the Additional Sample Attributes list.

An empty line appears in the list. (Figure 110)

Figure 110 Additional Sample Attributes list after adding new field					
Additional Sample Attributes (Opti Click "Add" to add other information	onal) i in additio	on to any attributes added from	the templates.		
Name	Туре	Value			
	Text 💌				
Delete Add					
(In the previous table, enter the Na	me and V	alue for your additional informat	ion: for example, if you wanted to collect a		
(In the previous table, enter the Name and Value for your additional information; for example, if you wanted to collect a comment, you might set the Name to "Comment" and the Value to "Here is my comment.")					

- b. Enter the attribute name and value.
- c. Select an attribute type for the user attribute:
 - Text: text string
 - Number: Floating point or Integer
 - Date: Calendar data

The attribute type determines the sorts of comparisons you can perform during an advanced search. For more information, see "Sample attributes" on page 102 and "Advanced search" on page 67.

d. Repeat to add more attributes.

The Arrays list (Figure 111) enables you to assign an array or set of arrays to the Sample (ARR) files.

	Fi	gure 111 A	Arrays list		
A	rra	ays		☑ Derive array names	from the sample file's name.
		Barcode		Probe Array Type (Required)	Array Name (Required)
		§5200637115004618	1701308401416533711	×	
		Lot Number: N/A	Expiration Date: N/A	Probe Array Position: N/A	
	D	elete Add			
Click "Add" to add an array to this sample file. To remove an array, select a check box next to an array and click "Delete". Checking "Derive array names from the sample file's name" will make the Array Names (which are used as base file names for DAT based on the Sample File Name. Entering or scanning a barcode will automatically set the Probe Array Type, if you have installed the appropriate library files. (The field.)					

You can include the following information on the array(s):

- Barcode (optional)
- Array Type
- Array Name

To assign an array to the Sample (ARR) file:

1. Enter the barcode (optional):

Enter the barcode using the keyboard; or

- a. Click in the Barcode field.
- b. Use the barcode reader to scan in the barcode on the array. (Figure 112)


The reader reads and sends the barcode to the Barcode field.

Note: You can use custom barcodes to register an array in Detailed Sample Registration.

The array's lot number and expiration date are displayed below the barcode (Applied Biosystems barcodes only).

Probe Array Position is an attribute for the GeneTitan System array plates and is not applicable to cartridge arrays.

2. Select the array type.

Note: If you are using Applied Biosystems barcodes, the array type is selected automatically after the barcode is entered. If you are using custom barcodes, you must select the array type manually.

The **Derive array names from sample names** check box is selected by default and an array name is created by linking:

- The Sample file name entered in the first set of steps
- The array type
- Incremental numbers added if necessary to distinguish arrays

F	Figure 113 Arrays list with array entered								
A	221/2		2 Derive array names from the cample file's name						
	Barcode Probe Array Type (Required) Array 1								
	≥5200637115004618	1701308401416533711	×						
	Lot Number: N/A	Expiration Date: N/A	Probe Array Position: N/A						
	Delete Ada	i)							
Click "Add" to add an array to this sample file. To remove an array, select a check box next to an array and click "Delete". Checking "Derive array names from the sample file's name" will make the Array Names (which are used as base file names for DAT Entering or scanning a barcode will automatically set the Probe Array Type, if you have installed the appropriate library files. (The E									

5

- 3. If you want to enter a different array name:
 - a. Deselect Derive array names from sample names check box.
 - b. Enter the name in the Array Name column.

To register additional arrays:

4. Click Add Array.

An empty line appears in the list. (Figure 114)

F	ig	ure 114 🥖	Array list with	second array added	
Π					
114	Arr	ays		⊻ Der	ive array names from the sample file's name.
Ш		Barcode		Probe Array Type (Required)	Array Name (Required)
Ш		@52006500461817	101308401416533711	HG-U133A_2	brain_03_(HG-U133A_2)
		Lot Number: 4014165	Expiration Date: 10/13/2008	Probe Array Position: N/A	
Ш				~	
		Lot Number:	Expiration Date:	Probe Array Position: N/A	
	(Delete A	dd		

The line enables you to enter data on an array.

5. After you have entered arrays, click **Save**.

A Sample file has been successfully saved message appears. (Figure 115)

6. Click **OK**.

Sample File saved successfully.

Editing files and copying attributes

You can use the Detailed Sample Registration to:

- Edit data in the Sample (ARR) file
- Rename the Sample (ARR) file
- Change the Array name in the Sample file
- Copy attributes over to a new file

Opening the Detailed Sample Registration page for a Sample file

- Click the Sample file link in the Folder View or Search Results pages.
- While displaying information about a Sample file in the Project view, click the **Open** button.

If there are template and attribute discrepancies, the Sample Attributes Conversion page will open.

See "Sample attributes conversion" on page 115 for more information about what you should do.

There are additional controls in the page when you have opened a previously created Sample file.

The **Rename** button enables you to change the name of the Sample file or array.

The **Save As** button copies the sample attribute and array type information over to a new Detailed Registration page which can be used to create a new file.

If you have made changes in a template used for the array file since creating the array file, you will see a notice and the **Update** button at the top of the Detailed Sample Registration page.

Figure 116 Warning message and Update button	
Detailed Sample Registration 🛙 - C:\Command_Console\Data\Dr Moriarty\brain_03.ARR	
WARNING: Either the template associated with the selected Sample file is missing, or the "type" (Text, Number, etc.) for one or more of the attributes in a template has changed since the Sample file was created.	Update 🗙
Sample File Name (Required): brain_03 Rename Save As	

Click the **Update** button to review the differences between the attributes and to correct the problem.

See "Sample attributes conversion" on page 115 for more information.

Editing the sample attributes in a sample file

- 1. Open the Sample file in the Detailed Sample Registration page.
- 2. Edit the attributes as desired.

Note: You cannot edit the barcode or array type information after an array has been scanned.

3. Click the Save button.

A notice that the Sample file has been successfully saved appears in a dialog box. (Figure 117)

Figur Save	e 117 Sample File d notice
1	Sample File saved successfully.
	ок

Renaming the sample file

IMPORTANT! If the **Derive Array Name from Sample File** check box is selected, changing the Sample file name will require changing the names of all the data files associated with the Sample file.

Renaming a Sample (ARR) file

- 1. Open the file in the Detailed Sample Registration page.
- 2. Click the **Rename** button next to the Sample File Name at the top of the page.
- 3. The Sample name can now be edited, and the Save button at the bottom of the page is replaced by the Rename button.
- 4. Enter a new name for the Sample file.
- 5. Make other changes as necessary.
- 6. Click Rename.

The Rename Sample File page opens with list of the DAT and CEL files that will be renamed. (Figure 118)

Figure 118 Rename Sample page									
Search Files By: 😰 Array Name 🔽 (Use * for wildcard) 🧧 Advanced Search 🔅									
HOME DATA SAMPLES ADMINISTRATION HELP									
Rename Sample File									
You are about to rename the sample file - C:\Command_Console\Data\Dr Moriarty\Brain_03.ARR. Renaming a sample file automatically renames associated GRD, JPG and Cell Summary Report files (if they exist), as well as the following list of files:									
C:\Command_Console\Data\Dr Moriarty\Brain_03_(HG-U133A_2).DAT C:\Command_Console\Data\Dr Moriarty\Brain_03_(HG-U133A_2).CEL									
C:\Command_Console\Data\Dr Monarty\Bram_03_(HG-U133A_2).AUDI1									
Do you want to rename the sample file?									
Yes No									

7. Click **Yes** to rename the sample file.

The page displays a list of the files with the new names. (Figure 119)

Search Files By: 🖾 Array Name 💌	(Use * for wildcard) Advanced Search							
IOME DATA SAMPLES ADMINISTRATION HELP								
Rename Sample File								
Denoming counts fits generated the following measures								
Kenaming sample nie generated the following messages:								
C:\Command_Console\Data\Dr Moriarty\Brain_03_(HG-U133A_2).AUDI	11 was renamed to							
C: Command_Console/Data/Dr Moriarty/Cereorum_03_(HG-U133A_2).A	was renamed to							
C.Command_ConsoleDataDr Avonatyloram_02(10-0153A_2).DA1 was relatined to C.Command_ConsoleDataDr MoniatylCreshum 03 (HG-III33A_2).DAT								
C:Command_Console/Data/Dr Honarty/Cercin 03 (HG-U133A_2), DFG was renamed to								
C:\Command Console\Data\Dr Moriarty\Brain 03 (HG-U133A 2).JPG w	C:Command Console/Data/Dr Moriarty/Cerebrum 03 (HG-U133A 2), JPG.							
C:\Command_Console\Data\Dr Moriarty\Brain_03_(HG-U133A_2).JPG w C:\Command Console\Data\Dr Moriarty\Cerebrum 03 (HG-U133A 2).J	PG.							
C:\Command_Console\Data\Dr Moriarty\Brain_03_(HG-U133A_2).JPG w C:\Command_Console\Data\Dr Moriarty\Cerebrum_03_(HG-U133A_2).JJ C:\Command_Console\Data\Dr Moriarty\Brain_03_(HG-U133A_2).CEL v	PG. was renamed to							

Changing the array name(s) for a sample file

Changing the array name for a sample file results in renaming all the data files associated with the array.

This can be done while editing or renaming a file.

Renaming the array name(s) for a Sample file

- 1. Open the Sample file in the Detailed Sample Registration page.
- 2. Deselect the **Derive array names from sample file name** check box.
- Click in the Array name column of the array you want to rename. The Rename Notice appears. (Figure 120)

Figure 120 Rename notice	
Changing the array name, will change the array names in all of the files associated with th	is array.
ОК	

- 4. Click **OK** and edit the Array Name(s).
- 5. Click **Rename** or **Save** in the Detailed Sample Registration page.

The Rename Arrays page opens with a list of the files that will be renamed.

Figure 121 Rename Arrays page									
Search Files By: 🖬 Array Name 🗸 (Use * for wildcard) 2 Advanced Search 🔅									
HOME DATA SAMPLES ADMINISTRATION HELP									
Rename Arrays									
You are about to modify array names in the sample file - C:\Command_Console\Data\Dr Moriarty\Cerebrum_03.ARR. Modifying an array's name automatically renames associated GRD, JPG and Cell Summary Report files (if they exist), as well as the following list of files: C:\Command_Console\Data\Dr Moriarty\Cerebrum_03_(HG-U133A_2).DAT C:\Command_Console\Data\Dr Moriarty\Cerebrum_03_(HG-U133A_2).CEL C:\Command_Console\Data\Dr Moriarty\Cerebrum_03_(HG-U133A_2).AUDIT									
Do you want to rename Arrays?									

6. Click **Yes** to rename the arrays and the data files.

The page displays a list of the files with the new names. (Figure 122)

Figure 122 Rename Arrays page with notice of changed data files									
Search Files By: 😰 Array Name 💌 (Use * for wildcard) 🔁 Advanced Search 🕄									
HOME DATA SAMPLES ADMINISTRATION HELP									
Rename Arrays									
Renaming array names generated the following messages:									
C:\Command_Console\Data\Dr Moriarty\Cerebrum_03_(HG-U133A_2).AUDIT was renamed to									
C:\Command_Console\Data\Dr Moriarty\Cerebrum_03.AUDIT.									
C:\Command_Console\Data\Dr Moriarty\Cerebrum_03_(HG-U133A_2).DAT was renamed to C:\Command_Console\Data\Dr Moriarty\Cerebrum_03_DAT									
C:Command_Console/Data/Dr Monarty/Cerebrum_03.DA1. C:Command_Console/Data/Dr Monarty/Cerebrum_03_(HG-U133A_2).JPG was renamed to									
C:Command_Console/Data/Dr Monarty/Cerebrum_03_[HG-0135A_2).JPG was renamed to C:Command_Console/Data/Dr Moriarty/Cerebrum_03.JPG.									
C:Command_Console/Data/Dr Monarty/Cerebrum_03_JPG. C:Command_Console/Data/Dr Moriarty/Cerebrum_03_(HG-U133A_2).CEL was renamed to									
C:Command_Console/Data'Dr Moriarty'Cerebrum_03.CEL.									
1									

Copying file data over to new Sample (ARR) file

- 1. Open file in Detailed Sample Registration page.
- 2. Click the Save As button by the Sample File Name box.

The Sample File Name becomes editable and the Barcode information for the arrays is erased.

Note: The Save As button is not available for GeneTitan System sample files.

- 3. Enter a name for the new Sample file.
- 4. Edit the Sample Attribute information if desired.
- 5. Enter new Array Type and Barcode information.
- 6. Click the **Save** button.

The Sample File Saved notice appears. (Figure 123)

Figure 123 Sample File Saved notice
Sample File saved successfully.

Sample attributes conversion

You may see the Sample Attributes Conversion page when you try to open a Sample file for editing.

The Sample Attributes Conversion page appears when there is a discrepancy between the properties of an attribute in the Sample file and the properties of the attribute as defined in the current template.

Attribute conversion may be necessary if any of the following changes have been made in a template:

- The attribute has been deleted from the template.
- The entire template has been deleted from GCC.
- The data type for the attribute in the template is different from the data type in the Sample file.

The page displays the attributes with discrepancies and the conversion that will be applied to correct the discrepancy. Depending upon the type of discrepancy, the attribute will either:

- Be converted to a user attribute, with Text type.
- Have its attribute type changed to match the template.

Applying the conversions

- Review the conversions in the Original Attribute and Converted Attribute lists. The details are described in:
 - "Deletion of attribute or template" on page 115
 - "Change in attribute type" on page 117
- 2. Click **Yes** in the Sample Attributes Conversion page.

The Detailed Sample Registration page opens with the Sample file displayed.

The converted attributes will be displayed in the Detailed Sample Registration page, but the conversions will not be applied to the Sample file until you:

3. Click **Save** in the Detailed Sample Registration file.

The changes will be applied to the Sample file.

The attribute conversion may affect how you search for Sample files using that particular attribute in the Advanced search page. The sections below describe this in more detail.

For more information about templates and data types, see:

- "Sample attributes" on page 102
- "Working with templates" on page 328

Deletion of attribute or template

If the attribute has been removed from the template, or if the entire template has been deleted, the attribute in the Sample file will be converted to a user-defined Sample attribute. (Figure 124)

Figure 124 Attribute deleted from template (converted to user attribute)									
Original Attribute Converted Attribute									
Template Name Type Value Template Name T									
Sept_Template Age Number 35 Age [Sept_Template]									
Sept_Template Disease name Text tumor Disease name [Sept_Template]									
Do you wish to continue with the conversion and edit the Sample file?									

This is indicated by the blank cell in the Template column for the converted attribute. The new user attribute name will use the original attribute name with the original template name in square brackets to indicate the source, as in the example Disease Status [Sept_Template].

In case of a name conflict, the new user attribute will have an underscore-number (_1) added to the attribute name:

Disease Status 1 [Sept Template]

The user attribute will be listed in the No_Template attribute list in the Select Template drop-down list of the Advanced Search page. (Figure 125)

Figure 125 Ac attribute from the	lvanced Sear ne No Templa	ch: selecting a user ate list
Step 2: Specify sam	ple attributes to Select Attribute	filter the search results Select Comparison
🔲 No Template 🛛 🗸	Disease status [St 💙	Equal to: 🗸
Delete	a [test] Assay Type	
Results must match	Automation Flag Comment Disease status (Sent	ted attributes
C Results can match	Experiment Date (Dat Experiment Date (Tex	ted attributes
Step 3: Specify opti	Sample Date (Date) Sample Date (Text) Sample Name	earch results
	Sample Project	The first Direct
Type of results to	Sample User	Limit results to the Projects:
return:	Tissue [July_Templat	All Projects and Data Roots
ARR	Treated	Cancer 1
DAT		

If other Sample files still have the original template attribute, the template will be listed in the Select Templates list. (Figure 126)

5



When doing an advanced search, if you want to find Sample files having the previous attribute type and the current attribute type, you will need to select both attributes in the Select attributes section. (Figure 127)

Figure 127	Advanced Sea	rch, specifying	g converted and u	nconverted attrib	outes	
Step 2: Specify	sample attributes to	filter the search re	sults			
Select Temp	Select Template Select Attribute Select Comparison Enter Value(s)					
No Template	Age [Sept_Temp 🗸	Equal to: 🗸	30		(use * for wildcard)	
Sept_Template	Age (Number) (pr 🗸	Greater than: 💉	25			
Delete	Add					
C Results must match ALL of the selected attributes						
Results can m	atch ANY of the select	ted attributes				

For more information about performing searches, see "Advanced search" on page 67.

Change in attribute type

Each attribute in a template is assigned to one of the following data types:

- Text: Text string
- Number: Integer or floating point number
- Date: Calendar data
- SingleSelect: Presents a list of items for the user to choose

Beta Versions of GCC included other data types which are no longer available, such as:

- Integer
- Floating Point
- MultiSelect

The data type determines the type of value that can be entered, and the types of comparisons that can be performed during an Advanced Search.

In this case, the results of the Attribute conversion depends upon the original attribute data type and the new attribute data type in the template.

• If the data types are compatible, the sample attribute will be converted to the new data type.

The Sample Attributes Conversion page shows the old and new attribute data types. (Figure 128)

Figure	128 Conv	ersion de	etails						
	Origina	l Attribute				Converted Attrib	ite		
Template	Name	Туре	Required	Value	Template 🛄	Name	Туре	Required	 Attribute type changed in template
Default	Diagnosis Code	Number	No	20	Default	Diagnosis Code	Text	No	, ittinoito type enangea in template
Default	Parents Living	SingleSelect	No	Yes		Parents Living [Default]	Text	No No	² — Attribute deleted from template
	New Attribute	s from Tem	plates						
Template	Name	Туре	Required	Value					
Default	Toxin Exposure	SingleSelect							

If the data types are not compatible, the existing sample attribute will be added as a user attribute with the text data type.

This gives you the option of manually transferring the attribute value to the new template attribute and deleting the added user attribute.

The attributes are converted according to the rules in the table below.

Table 1 Conversion rules

Old Sample File Data Type	New Template Attribute data type	Results
Text	Number	The attribute is converted to user attribute.
	Date	The attribute is converted to user attribute
	SingleSelect	Attribute type converted if it matches to one of the items in the Selection list; otherwise the attribute is converted to user attribute.
Number	Text	Attribute type converted.
	Date	Attribute is converted to user attribute.
	SingleSelect	Attribute is converted to user attribute.
Integer and Float (no	Number	Attribute type converted.
tonger supported)	Text	Attribute type converted.
	Date	Attribute is converted to user attribute.
	SingleSelect	Attribute is converted to user attribute.
Date	Text	Attribute type converted.
	Number	Attribute is converted to user attribute.
	SingleSelect	Attribute is converted to user attribute.

5

Old Sample File Data Type	New Template Attribute data type	Results
SingleSelect	Text	Attribute type converted.
	Number	Attribute is converted to user attribute
	Date	Attribute is converted to user attribute
MultiSelect (no longer	Text	Attribute type converted.
supported)	Number	Attribute is converted to user attribute
	Date	Attribute is converted to user attribute
	SingleSelect	Attribute is converted to user attribute

Table 1Conversion rules

If the sample attribute has the data type changed, you will be able to find the attribute listed for the template in the Advanced Search screen. (Figure 129)

Figure 129 Ac attribute type	dvanced sea	rch, selecting new
Step 2: Specify sam	ple attributes t	o filter the search results
Select Template	Select Attribut	e Select Comparison
Cancer_01 🔽	Age 🗸	Equal to:
Delete A	Age Diagnosis Date	
Results must match	Gender Height	ted attributes
C Results can match	Tissue Involved	ted attributes
	Weight (Number) (cu	e'
Step 3: Specify opti	Weight (Text) (previo	earch results

If the attribute type is changed, but it remains in the template, the type of comparisons you can perform when searching for the attribute may change.

If converted to a user attribute, you will need to select the attribute from the No Template list in the Specify Sample Attributes section of the Advanced search (Figure 130).

Figure 130 Advanced Search: selecting converted attributes from a template							
Stop 2. Specify com	nla attributos te	filter the second recults					
Step 2. Specify sam	ipie attributes to	inter the search results					
Select Template	Select Attribute	Select Comparison					
Cancer_01 🗸 🗸	Age 🗸 🗸	Equal to: 🗸					
Delete A	Age Diagnosis Date						
 Results must match 	Gender Height	ted attributes					
C Results can match	Tissue Involved	ted attributes					
	Weight (Number) (cur Weight (Number) (ore						
Step 3: Specify opti	Step 3: Specify opti (Weight (Text) (previousearch results						

If other Sample files still have the original attribute type, the attribute will be listed with both the old and new attribute types.

5



- The current attribute type in the template will have (current type) appended to the attribute name
- The previous attribute type will have (previous type) appended to the attribute name.

When doing an advanced search, if you want to find Sample files with the previous attribute type and with the current attribute type, you will need to select both attributes in the Select attributes section. (Figure 131)

Fi	Figure 131 Advanced Search, specifying converted and unconverted attributes							
5	Step 2: Specify	/ sam	ple attributes to	filter the sear	ch res	sults		
	Select Template Select Attribute Select Comparison Enter Value(s)							
	Cancer_01	*	Diagnosis Date 🗸 🗸	Before date:	*	1/1/2007		
	No Template	*	Dlagnosis Data [C 🗸	Equal to:	*			(use * for wildcard)
	Delete	A	dd					
C	C Results must match ALL of the selected attributes							
0	Results can r	natch	ANY of the selec	ted attributes				

For more information about performing searches, see "Advanced search" on page 67.

Quick sample registration

The Quick Sample Registration enables you to create a set of Sample (ARR) files quickly with the following basic information for the Sample and Array:

- Probe Array Type
- Sample File Name and Array Name
- Project
- Barcode (optional)

Barcodes and sample attributes can be added later on using various editing options. For more information, see "Adding a barcode to a sample file" on page 142 and "Batch editing" on page 144.

Both the Sample (ARR) file and the array name will have the same value when using Quick Sample Registration. As an example, Sample1ARR will have a physical array entry called Sample1.

You can create up to 48 Sample (ARR) files (one AutoLoader carousel's worth) at a time.

Note: This function works best for registering arrays that are not part of a set. If your array set contains an A and B array then use Register or Batch Register to create sample files (ARR). In addition, you cannot use Quick Sample Registration to register arrays for GeneTitan MC instrument.

Creating a set of Sample files with basic information

1. From the Samples menu, select Quick Register.

The Quick Sample Registration page opens. (Figure 132)

5

Figure 132 Quick Sample Registration page							
Search Files By: 📓	Array Name 🔽	(Use * for wildcard)	vanced Search 🔅				
HOME DATA SAME	PLES ADMINISTRATION HELP						
Quick Sample Registration 💷 🖬							
Define Samples > Con	firm > Finish						
Number of sample files (A Step 2: To assign a proj Project : Step 3: Add Details.	Step 1: Select the number of Sample (.ARR) files to create: Number of sample files (ARR) to create: Step 2: To assign a project or Probe Array Type to all Samples use Drop downs (optional step) Project: Project: Step 3: Add Details. *Required information: Probe Array Type, Sample File Name and Project						
Array Name will be derive	ed by concatenating the Sample File Name and the	Probe Array Type					
Barcode	Probe Array Type*	Sample File Name*	Project*				
Delete Next							

2. Select the number of Sample (ARR) files to create. (Figure 133)

You can add up to 48 arrays (an AutoLoader Carousel's worth) during one quick registration operation.

Figure 133 Drop-down I	ist		
Search Files By: 🛍 🛛 Array Name 💌		(Use * for wildcard) 2 Adv:	anced Search 🧔
HOME DATA SAMPLES ADMINI	STRATION HELP		
Quick Sample Registration 💷 😫			
Define Samples > Confirm > Finish			
Step 1: Select the number of Sample (.AF Number of sample files (ARR) to create :	R) files to create: 💷		
Step 2: To assign a project or Probe A ¹ ₂ Project : Probe Arraa	Sype to all Samples use D	Drop downs (optional step) 🔟	
Step 3: Add Details.	ole File Name and Project		
Array Name will be derived by concatena	e Sample File Name and the	e Probe Array Type	n : .+
Delete 14	Nex	sample rue ivame	rojeci
21 21 22 24 26 26 27 28 28			

Select a number from the drop-down list.
 Blank array information lines appear in the Array list. (Figure 134)

Figure 134 Add Details section with added rows							
Step 1: Select the number of Sample (.ARR) files to create: Number of sample files (ARR) to create :							
Step 2: To assign a project or Probe Array Type to a Project : Probe Array Type :	all Samples use Drop downs (options)	nal step) 💷					
Step 3: Add Details. *Required information: Probe Array Type, Sample File N Optional information: Barcode	lame and Project						
Array Name will be derived by concatenating the Sample	File Name and the Probe Array Typ	e					
Barcode	Probe Array Type*	Sample File Name*	Project*				
	×		~				
Lot Number: Expiration Date:							
	×		~				
Lot Number: Expiration Date:							

3. Set default values for all projects and/or probe array types (optional):

Figure 135 Set Defaults						
Step 2: To assign a project or Probe Array Ty Project : Dr Moriarty Probe Array Type :	pe to all Samples	us V	e Drop downs (option	ıal step) 💷		
Step 3: Add Details. *Required information: Probe Array Type, Sample	7GComplex5umGeno Ag ATH1-121501	^	ct			
Optional information: Barcode Array Name will be derived by concatenating the S	ax26087_a_ref_dir Barley1 Bovine Citrus		I the Probe Array Type		D 1 4	
Barcode	Citrus_SNP DCNtaolOr510989		Array Type*	Sample File Name*	Project*	
Lot Number: Expiration Date:	E_coli_2 Ecoli GenomeWideSNP_5 GenomeWideSNP_6 HG-Focus		V		Dr Moriarty	
Lot Number: Expiration Date:	HG-U133_Plus_2 HG-U133A HG-U133A_2 HG-U133B					
Delete	HT-HG-U133A HuEx-1_0-st-ta1 Mapping250K_Nsp Mapping250K_Sty Mitochip_2 Mouse430_2 SCID204:H520188		lext			
	TAG_3 Test3 Test3_bens	~				

- a. Select a project for the Project drop-down list.
- b. Select a probe array type from the Probe Array Type drop-down list.

The selected projects and probe arrays appear in the Array list. (Figure 136)

You can change the values for any sample file later on. Selecting these options will not erase your previously entered values for probe array type and project.

Fi	Figure 136 Add Details section with default probe array and project selected								
Ste Pro	Step 2: To assign a project or Probe Array Type to all Samples use Drop downs (optional step) 💷 Project : Dr Morianty 💉 Probe Array Type : HGU133A_2 💉								
Ster *Re Opt Arra	p 3: Add Details. equired information: ional information: B ay Name will be de	Probe Array Type, Sample File N arcode rived by concatenating the Sample	lame and Project File Name and the Probe Array	Typ	be				
		Barcode	Probe Array Type*		Sample File Name*	Project	*		
			HG-U133A_2	۷		Dr Moriarty	~		
	Lot Number:	Expiration Date:							
			HG-U133A_2	~		Dr Moriarty	*		
	Lot Number:	Expiration Date:							

- 4. (Optional) Enter the barcode using the keyboard; or
 - a. Click in the Barcode box.
 - b. Hold a GeneChip probe array in front of the barcode reader and squeeze the trigger for approximately four seconds until you hear a beep.

Note: You can use custom barcodes to register an array in Quick Sample Registration. Also, the array's lot number and expiration date are displayed below the barcode (Thermo Fisher Scientific barcodes only).

- 5. Enter a name for the Sample (ARR) file and the Array name (used for the DAT, CEL, and CHP files).
- 6. Change the project or probe array type using the individual drop-down lists in the list.

	F	igure 137 Sample names e	ntered					
S	tep	3: Add Details.						
*]	Rei	quired information: Probe Array Type, Sample File N	Name and Project					
0	pti	onal information: Barcode						
A	rra	y Name will be derived by concatenating the Sample	File Name and the Probe Array Ty	ype	e			
		Barcode	Probe Array Type*	Sample File Name* Proje			ect*	
1			HG-U133A_2	•	Dr_Smith_01	Dr Moriarty	*	
		Lot Number: Expiration Date:						
1			HG-U133A_2	•	Dr_Smith_02	Dr Moriarty	*	
L		Lot Number: Expiration Date:	-		·			

- 7. To delete Sample (ARR) files you do not want:
 - a. Select the check box in the row.
 - b. Click Delete.
- 8. Click Next.
 - The Confirm page opens. (Figure 138)

Figure 138 Confirm page
Search Files By: 🔟 Array Name 💌 (Use * for wildcard) 🗧 Advanced Search 🔅
HOME DATA SAMPLES ADMINISTRATION HELP
Quick Sample Registration 💷
Define Samples > Confirm > Finish
Sample From Row Status
1 File C:\Command_Console\Data\Dr Moriarty\Dr_Smith_02.ARR already exists and will not be recreated.
2 Sample Dr_Smith_03 is of array type HG-U133A_2 and will be saved to project Dr Moriarty
If you have errors but wish to continue registering only the valid records click the Next button and only the valid records will created. Or you may make corrections.
Next

The page displays the status of the sample files, indicating any errors that would prevent the registration.

These errors can include

- Same Sample (ARR) file name
- Missing file name
- Other conflicts with previously registered arrays If errors appear for certain sample files, but other sample files are correct, you can click the **Corrections** link to return to the Quick Sample Registration page and correct the errors.
- 9. Click **Next** to register the valid sample (ARR) files.

The Finish page appears. (Figure 139)

Figure 139 Quick Sample Registration Finish	page
Search Files By: 😰 Array Name 💌	(Use * for wildcard) Advanced Search
HOME DATA SAMPLES ADMINISTRATION HELP	
Quick Sample Registration 🗳	
Define Samples > Confirm > Finish	
Status	
The sample C:\Command_Console\Data\Dr Moriarty\Dr_Smith_03.ARR was c	reated successfully. <u>Edit</u>
Start Instrument Control Modules:	
Scan Control	
Fluidics Control	
1	

Click the **Edit** link to open the Sample file in the Detailed Sample Registration page (see "Detailed sample registration" on page 104)

You can use the links in the lower left corner of the screen to open the GCC Scan Control or GCC Fluidics Control software for further processing of the arrays.



The batch registration features enable you to create multiple Sample (ARR) files with different information, entering data using a specially formatted batch registration file.

Custom barcodes can be used in batch registration.

Batch registration involves three different sets of steps:

- 1. "Downloading an empty batch registration file"
- Entering values for the arrays into the batch registration file.
 See "Entering values in the batch registration file" on page 126.
- Uploading the data in the batch registration file to create the Sample (ARR) files.
 See "Uploading the batch registration file" on page 130.

The batch registration file is downloaded as an Excel workbook.

Downloading an empty batch registration file

1. From the Samples menu, select **Batch Registration**. The Batch Sample Registration page opens. (Figure 140)

Search Files By: 💷 🛛 Array Name 🕑	(Us	e * for wildcard)	Advanced Search
ME DATA SAMPLES ADMINISTRATION HELP			
tch Sample Registration 💷 🔒			
eate and Upload Batch Registration File	Confirm > Finish		
tep 1: Create a blank batch registration file wit	n the desired attributes		
elect the templates with the attributes you wish t MIAME Sample Information Moriarty TestA	o use for the sample files. I		
r use with Excel or compatible application: eate a spreadsheet for 0 samples ptional)project set to v ptional)probe array type set to v d with template defaults. You can change the pro	oject and probe array type w	hen editing the	
ownload			
ep 2: Enter the values for the Sample (.ARR) f	les in the batch registration	n file.	
iter values for the attributes using Excel or a text w) of the spreadsheet defines which fields to coll w contains the information for one Sample (.ARR) n be added to the spreadsheet at any time.	-editing program. The first r ect. Each additional row belo file. Additional columns for	ow (the heading ow the heading new attributes	
ep 3: Upload the batch registration file to creat	e new sample (.ARR) files	•	
nter the path, or click Browse to find the batch req elimited .TXT) .	jistration file (.XLS) format o	or Tab	
Allow Custom Barcodes			
	Browse		
ick Upload to upload the Sample information. Upload			

 Select the templates you want to use by placing a check in the box next to their names. (Figure 141)

Figure 141 Select Templates (with	h attributes displayed for template)	
Step 1: Create a blank batch reg	jistration file with the desired attrib	utes
Select the templates with the attr	ibutes you wish to use for the sample	e files. 💷
 MIAME Sample Information Moriarty TestA 	TestA	
	gender	
	age	
	tissue type	
For use with Excel or compatible a Create a spreadsheet for 0 s (optional)project set to v (optional)probe array type set to and with template defaults. You c document.	pplication: amples an change the project and probe array	y type when editing the

You can display the attributes in the template by clicking on the template name.

- 3. Specify the number of samples. The maximum number of samples for which the downloaded worksheet works well is 1000.
- 4. Specify project and array type for the Sample files.
- 5. Click **Download** to download the Excel workbook.

When using GCC Portal, the Excel program displays the created workbook, which you can edit and save on your computer.

Entering values in the batch registration file

The Batch Registration file can be used to enter data for several different Sample (ARR) files at once.

The downloaded batch registration file is an Excel workbook with three worksheets:

- Samples worksheet, where you enter the data
- General info worksheet (do not edit), where GCC Portal stores information about Array types, projects, and file format
- Template Info worksheet (do not edit), where GCC Portal stores information about the template attributes.

Note: You cannot create TSV files in GCC 4.3, but you can use TSV files. created in previous versions of GCC to perform batch registration. For more in formation, see Appendix G, "TSV files" on page 372.

F	Figure 142 Batch Registration Workbook, Samples Worksheet								
	A	В	C	D	E	F	G	Н	
1	Sample File Path	Project	Sample File Name	Array Name	Probe Array Type	Barcode	gender:TestA:SingleSelect:Required	age:TestA:Number:Required	tissue type:TestA:Text
2		Dr Moriarty			HG-U133A_2				
3		Dr Moriarty			HG-U133A_2				
4		Dr Moriarty			HG-U133A_2				
5									
6									
7									
8					-				
H	< ▶ ▶\\Samples (D	O_NOT_EDIT	/ DO_NOT_EDIT_TEM	PLATE_INFO ,	/		<	IIII	

The columns in the Samples worksheet have column headers that define the information on the Sample files, the physical array, and the attributes:

Sample File Path	The path to where the Sample file will be created. Can be used to place Sample files in project folders.
Project	The project that the Sample (ARR) file will be assigned to.

Note: You must specify either the **Path** or **Project** for your files. Specifying both will produce an error message.

Sample File Name	Unique identifier for the Sample file.
Array Name	Name assigned to the array during registration.
Probe Array Type	Part number for the array(s).
Barcode	Barcode on the array(s).
Attributes	Additional information about the sample and experiment that you can use to interpret your results.

Path

The path needs to be associated with a data root. You can assign a set of sample files to a particular project if you select that project's folder in the Path field.

Project

Specifying a project for the Sample file will determine the folder the Sample file is created in.

You can select the project from a drop-down list. (Figure 143)

Figure 143 List of projects							
A	В	С					
Path	Project	Sample File Name	Array Ւ				
	Build37EU133a	▼tch1	Batch1				
	Build37EU133a	itch2	Batch2				
	Default New Project3	tch3	Batch3				
	Plus2						

Sample file name

Enter the name assigned to the Sample file that will be created.

Array name, array type, and barcode

If you are using Excel, you can select the probe array type from a drop-down list. (Figure 144)

Figure 144 List of probe arrays						
E	F					
Probe Array Typ	Barcode	Sample				
HG-U133A	-	Batch1				
HG-U133A	~	Batch2				
HG-U133A_2		Batch3				
HT HG-U133A						
Mapping50K_Hind24	=					
Mapping50K_Xba24						
Test3	-					
Dens						
	1					

You can also enter multiple array information for a single sample file.

Entering multiple arrays

- 1. Enter the sample file information (File path, project, and file name) on a separate line of the worksheet for each array you want to use.
- 2. Enter a different array name for each array for the sample.
- 3. Select the array type from the Probe Array Type list.
- 4. Enter the array barcodes in the appropriate lines.
- 5. Make sure that the attributes are the same for all sample entries.

F	Figure 145 Worksheet with multiple arrays entered for samples									
	A	В	C	D	E	F	G	Н	1	
1	Sample File Path	Project	Sample File Name	Array Name	Probe Array Type	Barcode	gender:TestA:SingleSele	age:TestA:Number:Req	tissue type:TestA:Text	
2		asdf	X_Sample_01	X_Sample_01_A	HG-U133A		M	34	Brain	
3		asdf	X_Sample_01	X_Sample_01_B	HG-U133B		M	34	Brain	
4		asdf	X_Sample_02	X_Sample_02_A	HG-U133A		M	35	Liver	
5		asdf	X_Sample_02	X_Sample_02_B	HG-U133B		M	35	Liver	
6		asdf	X_Sample_03	X_Sample_03_A	HG-U133A		F	44	Kidney	
7		asdf	X_Sample_03	X_Sample_03_B	HG-U133B		F	44	Kidney	
8										

5

Attributes

Enter the values for the attributes in the appropriate columns.

You can select the value for a SingleSelect attribute from a drop-down list. (Figure 146)

Figure 146 Selecting the value for a SingleSelect attribute							
i	Н						
Name:D	Gender:Defau	Weight:Defau					
	F	50					
	F	40					
	F	- 30					
M							

GCC uses two types of attributes for Batch Registration:

- Template Attributes: Attributes that have been defined in a template. When you select templates for the downloaded batch registration file, the array attributes in those templates will be included as headings in the batch registration file.
- User Attributes: Attributes that you add in the Batch Register file. You create a user attribute by entering the attribute name and other characteristics in the column header, and then entering attribute values in the appropriate cells.

Attributes need to have the following characteristics defined:

Fig	gure 147 Template and	user attributes in t	he Batch Edit file
	H		J
	age:TestA:Number:Required	tissue type:TestA:Text	disease:*:Text
	35	brain	cancer
	35	brain	cancer
	42	Liver	TB
	41	lung	lupus
	Template At	tributes	User Attribute

- AttributeName
- TemplateName (if any; not used for User Attributes)
- DataType
- Required status, if any

The column headings are in the format:

• Header format for Template Attribute: AttributeName:TemplateName:AttributeType:RequiredStatus

• Header format for User Attribute: AttributeName:*:AttributeType

Uploading the batch registration file

1. Enter the file path and name in the text box (Figure 148) or click **Browse**.

Figure 148 Upload file

Step 3: Upload the batch registration file to create new sample (.ARR) files.

Enter the path, or click Browse to find the batch registration file (.XLS) format or Tab delimited .TXT) .

Allow Custom Barcodes

C:\Documents and Settings\rallso\Desktop\Downloads\BatchRegistration_2.xls Browse...

Click Upload to upload the Sample information.

Upload

- Clicking **Browse** opens a Choose File window.
- Select the Batch Registration file and click **Open**.
 The file and its path is displayed in the box.
- 2. Click the **Allow Custom Barcodes** check box to use barcodes that are not provided by Applied Biosystems.
- 3. Click **Upload**.

If there are problems with the workbook, an error notification page appears. (Figure 149)

Figure 149 Error notification
Search Files By: Array Name Array Name Array Name Array Name Advanced Search
Batch Sample Registration 🖬
Create and Upload Batch Registration File > Confirm > Finish
Errors:
Unable to consolidate the sample at the row 2. The column "gender:TestA:SingleSelect:Required" has different value or type for the same sample attribute of the sample file "C:\Command_Console\Data\Dr Moriarty\X_Sample_01.ARR".
You have errors but if you wish to continue editing only the valid records click the Save button and only the valid records will be edited. Or you may cancel the process by clicking Cancel.
Cancel

The error messages indicate problems such as bad barcodes, problems with registering multiple arrays on a sample, etc.

• Click Cancel to cancel the registration and fix the problems; or

Click **Save** to register the valid records.

If the upload doesn't have a problem the Folders View page appears with the newly created folders.

Sample prep plate registration

Sample Prep Plate Registration provides a convenient way to register samples and cartridge arrays for up to two 96-well plates by using an Excel workbook.

To perform Sample Prep Plate Registration for a target prep plate:

- 1. "Downloading the sample prep plate registration file", below
- 2. "Entering data in the workbook" on page 132
- 3. "Uploading the data for the files" on page 132

1. From the Samples menu, select Sample Prep Plate Registration.

The Sample Prep Plate Registration page appears (Figure 150).

Downloading the sample prep plate registration file

Figure 150 Sample Prep Plate Registration page		
Search Files By: 🔟 Array Name 💌	(Use * for wildcard) Advanced Search	٩
HOME DATA SAMPLES ADMINISTRATION HELP		
Sample Prep Plate Registration 💷 🖬		
Create and Upload Sample Prep Plate Registration File > Confirm > Finish		
Step 1: Create a blank Sample Prep Plate Registration file.		
Download		
Dowindad		
Step 2: Enter the values for the Sample (.ARR) files in the Sample Prep Plate Registra	ition	
file.		
Enter values for the attributes using Excel or a text-editing program. The file reflects a 96- plate. Columns are A-H and Rows are 1-12. A sample name and GeneChip barcode must be given for each well position for which a Sample (.ARR) file is to be created.	-well	
Step 3: Upload the Sample Prep Plate Registration file to create new sample (.ARR) fi	iles.	
Enter the path, or click Browse to find the Sample Prep Plate Registration file (.XLS format	.).	
Brows		
Create files in this project: Batch_Register_Test		
Plate ID for first tab (optional)		
Plate ID for second tab (optional)		
Click Upload to upload the information.		
υριοαα		
Mouse over 🛄 for tips on step.		

2. Click **Download** to create a blank Sample Prep Plate Registration file.

The Excel program displays the created workbook, which you can edit and save on your computer.

Entering data in the workbook

Entering data for the Sample Prep Plate Registration file

• Enter a sample (ARR) file name and GeneChip barcode for each well position you are analyzing using Excel or text-editing software.

The blank Sample Prep Plate Registration file (Figure 151) is an Excel workbook with two tabs, to enable use with arrays that require two prep plates.

The worksheet rows are marked A through H, corresponding to the plate rows. The worksheet columns are marked 1 through 12, corresponding to the plate columns.

Figure	Figure 151 Excel File for the target prep plate												
A	В	C	D	E	F	G	н		J	К	L	M	
1 Header	1	2	3	4	5	6	7	8	9	10	11	12	
2 A Sample													
3 A Barcode		1											
4									-				_
6 B Sample													_
6 B Barcode													-
1 C Commis													_
8 C Sample										7	2		_
9 C Barcode													_
11 D Sample													-
12 D Barcode										1			<u> </u>
13		-											- 1
14 E Sample													_
15 E Barcode													
16			2										
17 F Sample													
18 F Barcode													
19													
20 G Sample													
21 G Barcode													
22									1		1		_
23 H Sample													
24 H Barcode													-
26				-									
H + + H Sheet	1 / Sheet2 / S	Sheet3 /	1	1	1	1	1	<	1	ш			2

For each well position, enter the Sample name for the Sample (ARR) and the barcode for the probe array.

Uploading the data for the files

1. From the Samples menu, select Sample Prep Plate Registration.

The Sample Prep Plate Registration page appears.

- 2. Enter the path or click **Browse** to select the plate registration file.
- 3. Select a project for the Sample (ARR) files (optional).
- 4. Enter plate IDs if registering samples for two plates.

The Array names will be based on the Sample Name entered in the worksheet, concatenated with the plate ID, if any, and the Well position as indicated by their position in the worksheet.

5. Click Upload.

The Confirm page appears. (Figure 152)

5

Figure 152 Confirm page					
Search File:	s By: 🔟 🛛	Array Name 💌	(Use * for t	wildcard) 🖻 <u>Adva</u> r	nced Search
HOME DATA SAMPLES ADMINISTRATION HELP					
Sample Prep Plate Registration 🗉					
Create and Upload GeneTitan Sample Registration File > C	onfirm	> Finish			
The following samples have been read from the file.					
File Name F	tow Colu	nn Sample Name	Barcode	Array Name	Message
C:\Command_Console\Data\Default\Sample_Plate_01.ARR.4	1	Sample_Plate_01	@5200650046181710130840141653371	.5Sample_Plate_01_	Sample successfully read from file.
C:\Command_Console\Data\Default\Sample_plate_02.ARR.4	2	Sample_plate_02	@5200650046181710130840141653371	.6 Sample_plate_02_	Sample plate1_A_2 successfully read from file.
C:\Command_Console\Data\Default\Sample_Plate_03.ARR.A	3	Sample_Plate_03	@5200650046181710130840141653371	7Sample_Plate_03_	Sample plate1_A_3 successfully read from file.
C:\Command_Console\Data\Default\Sample_Plate_04.ARR.A	4	Sample_Plate_04	@5200650046181710130840141653371	.8 Sample_Plate_04_	Sample plate1_A_4 successfully read from file.
If you have errors but wish to continue registering only the may cancel the process by clicking Cancel.	valid recc	rds click the Save bu	utton and only the valid records will uplo	oad. Or you	

The page displays a list of the Sample (ARR) files created for the plate, along with Sample name, barcodes, and array names.

Error messages are displayed if there is a problem. These errors must be corrected before finishing the registration.

If there are any errors:

- a. Click Cancel
- b. Check the plate worksheet.
- c. Proceed with the upload again.
- 6. Click Next.

The Finish page opens. (Figure 153)

5

Figure 153 Finish page				
Search File	s By: 💷 🖟	Array Name 💌	(Use * for wildcard) 🛛 Advanced S	earch 🍳
HOME DATA SAMPLES ADMINISTRATION HELP				
HT Sample Registration 🖻				
Create and Upload Batch Registration File > Confirm > Fil	nish			
The following samples have been read from the file.				
File Name F	Row Colui	nn Sample Name Barcode	Array Name	Message
C:\Command_Console\Data\Default\Sample_Plate_01.ARR	4 1	Sample_Plate_01 @52006500461817101308	3401416533715 Sample_Plate_01_plate1	_A_1 successfully uploaded.
C:\Command_Console\Data\Default\Sample_plate_02.ARR	4 2	Sample_plate_02@52006500461817101308	3401416533716 Sample_plate_02_plate1	Sample _A_2 successfully uploaded.
C:\Command_Console\Data\Default\Sample_Plate_03.ARR#	4 З	Sample_Plate_03 @52006500461817101308	3401416533717 Sample_Plate_03_plate1	Sample _A_3 successfully uploaded.
C:\Command_Console\Data\Default\Sample_Plate_04.ARR#	4 4	Sample_Plate_04@52006500461817101308	3401416533718Sample_Plate_04_plate1	Sample _A_4 successfully uploaded.
Batch Array Registration is compl	ete.			

Click **Create Summary Spreadsheet for Batch Edit** to open the Summary page and create a workbook summary of the Sample files that can be used for batch editing the Sample (ARR) files.

GeneTitan array plate registration

GeneTitan Array Plate Registration provides a convenient way to register samples and plate arrays for an Array Plate by using an Excel workbook.

A 384 or Mini 96 array plate can be used. A 96 array plate (Figure 154) may contain 16, 24, or 96 arrays. A Mini 96-array plate contains 96 arrays on a 384 format.

These formats allow for increased automation and processing times for large array counts.



The array plate has a barcode for tracking. Each individual array on the plate is identified by its row and column. For example, the circled array in the figure below is array D05.



There are three sets of steps:

- "Downloading the GeneTitan array plate workbook", below.
- "Completing the workbook" on page 138.
- "Uploading the workbook" on page 139.

Downloading the GeneTitan array plate workbook

Downloading the Excel Workbook

 From the Samples menu, select GeneTitan Array Plate Sample Registration. The GeneTitan Array Plate Sample Registration page appears (Figure 156).

The path, or click Browse to find the GeneTitan Array Plate registration file to create new sample (.ARR) files. Enter the path, or click Browse to find the GeneTitan Array Plate registration file. If a plate barcode is not provided in the excel file being uploaded, one MUST be provided in the plate barcode field below. GeneTitan Array Plate Barcode: Upload Mouse over I for tips on step.	Figure 156 GeneTitan Array Plate Registration page
Conception of the sample (.ARR) files in the GeneTitan Array Plate registration file. Step 2: Enter the values for the sample (.ARR) files in the GeneTitan Array Plate registration file. Step 3: Upload the GeneTitan Array Plate registration file to create new sample (.ARR) files. Step 3: Upload the GeneTitan Array Plate registration file to create new sample (.ARR) files. Step 3: Upload the GeneTitan Array Plate registration file (Required): GeneTitan Array Plate registration file (Required): GeneTitan Array Plate registration file (Required): Upload Mouse over if for tips on step.	
GeneTitan Array Plate Registration III IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	- □ × ⊕ ⊕ ■ http://localhost8000/AffyWeb/RegisterHTArray P ~ C ■ Register GeneTitan Array PL × Search Files By: ■ Array Name ✓ (Use * for wildcard) ■ Advanced Search HOME DATA SAMPLES ADMINISTRATION HELP
Step 1: Create a blank GeneTitan Array Plate registration file with the desired attributes Select the templates with the attributes you wish to use for the sample files. I > IMIAME Sample Information > Dedigree Template GeneTitan Array Plate Type (Required): 384_AMMS-384 V Project where to create samples: Download Step 2: Enter the values for the sample (.ARR) files in the GeneTitan Array Plate registration file. Enter values for the attributes using Excel. Additional columns for new attributes can be added to the spreadsheet at any time. I Step 3: Upload the GeneTitan Array Plate registration file to create new sample (.ARR) files. Enter the path, or click Browse to find the GeneTitan Array Plate registration file. If a plate barcode is not provided in the excel file being uploaded, one MUST be provided in the plate barcode field below. GeneTitan Array Plate registration file (Required): Browse GeneTitan Array Plate Barcode: Upload Mouse over I for tips on step. Mouse over I for tips on step.	GeneTitan Array Plate Registration 🗉 🖻
Select the templates with the attributes you wish to use for the sample files. > MIAME Sample Information > Project Marker Sample Information Project where to create samples: Download Step 2: Enter the values for the sample (.ARR) files in the GeneTitan Array Plate registration file. Enter values for the attributes using Excel. Additional columns for new attributes can be added to the spreadsheet at any time. Step 3: Upload the GeneTitan Array Plate registration file to create new sample (.ARR) files. Enter the path, or click Browse to find the GeneTitan Array Plate registration file. If a plate barcode is not provided in the excel file being uploaded, one MUST be provided in the plate barcode field below. GeneTitan Array Plate registration file (Required): GeneTitan Array Plate Barcode: Upload Mouse over I for tips on step.	Step 1: Create a blank GeneTitan Array Plate registration file with the desired attributes
GeneTitan Array Plate Type (Required): 384_AIMS-384 Project where to create samples: Download Step 2: Enter the values for the sample (.ARR) files in the GeneTitan Array Plate registration file. Enter values for the attributes using Excel. Additional columns for new attributes can be added to the spreadsheet at any time. Step 3: Upload the GeneTitan Array Plate registration file to create new sample (.ARR) files. Enter the path, or click Browse to find the GeneTitan Array Plate registration file. If a plate barcode is not provided in the excel file being uploaded, one MUST be provided in the plate barcode field below. GeneTitan Array Plate registration file (Required): GeneTitan Array Plate Barcode: Upload Mouse over I for tips on step.	Select the templates with the attributes you wish to use for the sample files. ■
Download Step 2: Enter the values for the sample (.ARR) files in the GeneTitan Array Plate registration file. Enter values for the attributes using Excel. Additional columns for new attributes can be added to the spreadsheet at any time. Step 3: Upload the GeneTitan Array Plate registration file to create new sample (.ARR) files. Enter the path, or click Browse to find the GeneTitan Array Plate registration file. If a plate barcode is not provided in the excel file being uploaded, one MUST be provided in the plate barcode field below. GeneTitan Array Plate registration file (Required): Browse GeneTitan Array Plate Barcode: Upload	GeneTitan Array Plate Type (Required): 384_AIMS-384 V Project where to create samples: V
Enter values for the attributes using Excel. Additional columns for new attributes can be added to the spreadsheet at any time. Step 3: Upload the GeneTitan Array Plate registration file to create new sample (.ARR) files. Enter the path, or click Browse to find the GeneTitan Array Plate registration file. If a plate barcode is not provided in the excel file being uploaded, one MUST be provided in the plate barcode field below. GeneTitan Array Plate registration file (Required): GeneTitan Array Plate Barcode: Upload Mouse over I for tips on step.	Download Step 2: Enter the values for the sample (.ARR) files in the GeneTitan Array Plate registration file.
Enter the path, or click Browse to find the GeneTitan Array Plate registration file. If a plate barcode is not provided in the excel file being uploaded, one MUST be provided in the plate barcode field below. GeneTitan Array Plate registration file (Required): GeneTitan Array Plate Barcode: Upload Mouse over I for tips on step.	Enter values for the attributes using Excel. Additional columns for new attributes can be added to the spreadsheet at any time.
GeneTitan Array Plate registration file (Required): GeneTitan Array Plate Barcode: Upload Mouse over II for tips on step.	Enter the path, or click Browse to find the GeneTitan Array Plate registration file. If a plate barcode is not provided in the excel file being uploaded, one MUST be provided in the plate barcode field below.
GeneTitan Array Plate Barcode:	GeneTitan Array Plate registration file (Required): Browse
Upload Mouse over II for tips on step.	GeneTitan Array Plate Barcode:
Mouse over 🔲 for tips on step.	Upload
Mouse over 🔲 for tips on step.	
	Mouse over 🔟 for tips on step.

2. Select the templates you want to use by placing a check in the box next to their names (Figure 157).

Figure 157 Select Templates
Step 1: Create a blank GeneTitan Array Plate registration file with the desired attributes
Select the templates with the attributes you wish to use for the sample files. ■
GeneTitan Array Plate Type (Required): HT_GenomeWide_6_p1-24 💌
Project where to create samples:
Download

You can display the attributes in the template by clicking on the template name.

- 3. Specify the GeneTitan Array Plate type and the project for the Sample files (required).
- 4. Click **Download** to download the file.

The Excel program displays the created workbook, which you can edit and save on your computer.

5

Completing the workbook

The Batch Registration file can be used to enter data for all of the plate arrays on an array plate in one operation.

The downloaded workbook has three worksheets:

- Samples worksheet, where you enter the data
- General info worksheet (do not edit), where GCC Portal stores information about Array types, projects, and file format
- Template Info worksheet (do not edit), where GCC Portal stores information about the template attributes

Figure 158 Excel file for Batch GeneTitan Array Plate Registration

GeneTitanArrayPlate	Registration.xls	[Compatibility Mod	e]							
A	B	С	D	E	F	G	H	I. I.	J	K
Sample File Path	Project	Plate Type	Probe Array Type	Probe Array Position	Barcode	Sample File Name	e Array Name	gender:TestA:SingleSelect:Required	age:TestA:Number:Required	tissue type:TestA:Tex
	Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	A05	5500014037284120308255	Sample_AA	Array_AA	M	34	
	Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	A07	5500014037284120308255	Sample_AB	Array_AB	F	76	
	Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	A09	5500014037284120308255	Sample_AC	Array_AC	M	34	
	Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	B05	5500014037284120308255	Sample_AD	Arrau_AD	M	67	
	Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	B07	5500014037284120308255	Sample_AE	Array_AE	F	72	
	Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	B09	5500014037284120308255	Sample_AF	Array_AF	M	56	
	Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	C05	5500014037284120308255	Sample_AG	Array_AG	M	23	
	Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	C07	5500014037284120308255	Sample_AH	Array_AH	F	76	
	Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	C09	5500014037284120308255	Sample_Al	Array_Al	M	34	
	Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	D05	5500014037284120308255	Sample_AJ	Array_AJ	M	67	
	Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	D07	5500014037284120308255	Sample_K	Array_K	F	45	
	Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	D09	5500014037284120308255	Sample_AL	Array_AL	M	54	
	Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	E05	5500014037284120308255	Sample_AM	Array_AM	M	34	
	Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	E07	5500014037284120308255	Sample_AN	Array_AN	F	76	
	Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	E09	5500014037284120308255	Sample_AO	Array_AO	M	34	
	Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	F05	5500014037284120308255	Sample_P	Array_P	M	67	
	Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	F07	5500014037284120308255	Sample_AQ	Array_AQ	F	45	
	Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	F09	5500014037284120308255	Sample_R	Array_R	M	54	
	Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	G05	5500014037284120308255	Sample_AS	Array_AS	M	34	
	Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	G07	5500014037284120308255	Sample_AT	Array_AT	F	76	
	Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	G09	5500014037284120308255	Sample_AU	Array_AU	M	34	
	Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	H05	5500014037284120308255	Sample_AV	Array_AV	M	67	
	Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	H07	5500014037284120308255	Sample_W	Array_W	F	45	
	Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	H09	5500014037284120308255	Sample_X	Array_X	M	54	

The Sample worksheet has columns with headers that define the property being entered.

Some properties define the sample and data files file and the physical array:

Sample File Path	The path to where the Sample file will be created. Can be used to place Sample files in project folders.
Project	The project that the Sample (ARR) file will be assigned to.
Plate Type	Model of array plate.
Probe Array Type	The array type on the plate.
Probe Array Position	Column and row position for the plate array.
Barcode	Plate barcode: can be entered when you upload the batch registration file.
Sample File Name	Name to be used for the Sample (ARR) file.
Array Name	Name to be used for the array plate and for all the data files (DAT, CEL, and CHP)
Attributes	Additional information about the sample and experiment that you can use to interpret your results.



Path

The path needs to be associated with a data root. You can assign a set of sample files to a particular project if you select that project's folder in the Path field.

Project

Specifying a project for the Sample file will determine the folder the Sample file is created in.

If you are using Excel, you can select the project from a drop-down list. (Figure 143)

Figure 1 workboo	59 List of pr ok	ojects in Excel	
A	В	С	
Path	Project Build37EU133a Default New_Project3 Plus2	Sample File Name tch1 tch2 tch3	Array N Batch1 Batch2 Batch3

Plate type, probe array type, probe array position

These items specify the array plate type, the plate array type, and the array plate position.

They are automatically filled out when you create the plate batch workbook file.

File names

Enter the name assigned to the Sample file that will be created.

Barcode

This is the array plate barcode; if you enter a barcode into the A05 probe array position barcode cell, the same barcode is copied automatically into all of the other rows.

Sample file and array name

Enter the names to be used for:

- The Sample (ARR) file.
- The Array plate and for all the data files (DAT, CEL, and CHP) for the array on the Array Plate.

Attributes

Enter the values for the attributes in the appropriate columns. See "Attributes" on page 129 for more information.

Uploading the workbook

- From the Samples menu, select GeneTitan Array Plate Registration. The GeneTitan Array Plate Sample Registration page appears (Figure 156).
- 2. Enter the file path and name in the Registration file box (Figure 160); or



3. Click Browse.

The Choose File window appears.

4. Click to select the array plate registration file, then click **Open**.

The file and its path is displayed in the Registration file box.

Note: If the plate barcode did not auto-populate, enter it now.

5. Click Upload.

If there are problems, the Errors page appears. (Figure 161)

Figure 161 Error notice
Search Files By: 🗉 🛛 Array Name 💌 📃 (Use * for wildcard) 🧧 Advanced Search 🎈
HOME DATA SAMPLES ADMINISTRATION HELP
Confirm GeneTitan Arrays Plate Sample Registration 💷 - GeneTitanArrayPlateRegistration.xls
Errors:
Cannot read sample (Sample_AF) in row 7 of Excel file. Required attribute 'age' is empty Cannot read sample (Sample_AG) in row 8 of Excel file. Required attribute 'age' is empty
Unable to register GeneTitan Array Plate Samples. Please correct the above errors and retry uploading the GeneTitan Array Plate sample file.
Cancel

Click Cancel in order to correct problem(s) before uploading.

IF there are no problems, the Confirm Batch Sample Registration page opens. (Figure 162)

5

Figure 162 Confirm Batch Sample Registration
Search Files By: 🛙 Array Name 🔄 🛛 (Use * for wildcard) 🧧 Advanced Search
HOME DATA SAMPLES ADMINISTRATION HELP
Confirm GeneTitan Arrays Plate Sample Registration 💷 - GeneTitanArrayPlateRegistration.xls
GeneTitan Array Plate Registration file has been loaded without any errors. Do you want to save samples?
bene nar ningy nate negistration me has been loaded without duy chois, bo you want to sure sumples.
Cancel Save

6. Click **Save** to register the valid records.

The page displays a message that the Batch Sample Registration is complete. (Figure 163)

	Figure 163 Confirmation page, upload successful
_	
	Search Files By: 📓 Array Name 💌 🛛 (Use * for wildcard) 🧧 Advanced Search
	HOME DATA SAMPLES ADMINISTRATION HELP
	Confirm GeneTitan Arrays Plate Sample Registration 🛽 -
	Registered GeneTitan Array Plate Samples successfully.

Adding a barcode to a sample file

You may not have the barcode available when the Sample file is first created; if so, you can add it later using the Add Barcode page.

Note: The Add Barcode page can only be used to add one barcode at a time. The Batch Edit workbooks can be used to add barcodes to multiple sample files or multiple barcodes to one sample file in a single operation (see "Batch editing" on page 144). The Add Barcode page cannot be used to add a barcode for a Array Plate. Array Plate barcodes must be provided at the time of registration

1. From the Samples menu, click Add Barcode.

The Add Barcode window opens. (Figure 164)

Search Files By: 📓 Array Name 💌			
Search Files By: Array Name			
	(Use * for wildcard)	Advanced Search	4
OME DATA SAMPLES ADMINISTRATION HELP			
.dd Barcode to Array 😰			
Step 1: Scan the barcode of the Array			
Scan the barcode of the array and press the 'Search Arrays' button to see Sam	ple files that need an array of the ty	rpe scanned.	
Array bacoda	Search Arrays		

2. Enter the barcode:

Enter the barcode using the keyboard; or

- a. Click in the Barcode field.
- b. Use the barcode reader to scan in the barcode on the array.

The reader reads and sends the barcode to the Barcode field.

3. Click Search Arrays.

A list of Array names for that type of array that need a barcode appears in the Array list. (Figure 165)

Figure 165 Sample files displayed						
Search Files By: 🛙 Array Name 💌			(Use * for wildca	ard) 🖻 <u>Advance</u>	d Search 🔅	
HOME DATA SAMPLES ADMINISTRATION HELP						
Add Barcode to Array 🙆						
Step 1: Scan the barcode of the Array						
Scan the barcode of the array and press the 'Sear Array barcode: @520065004618171013064014165	Scan the barcode of the array and press the 'Search Arrays' button to see Sample files that need an array of the type scanned.					
Associated Probe Array Types: HG-U133A_2						
Step 2: Select the Array to add the barcode						
Selected File Name Project Name	Array Name B	arcode Lot Numbe	Expiration Date	Probe Array Type	Date Modified	
Patient_02.ARR Batch_Register_Test	Patient_02			HG-U133A_2	1/29/2008 12:57:44 PM	
Patient_04.ARR Batch_Register_Test	Patient_04			HG-U133A_2	1/29/2008 12:57:44 PM	
Patient_05.ARR Batch_Register_Test	Patient_05			HG-U133A_2	1/29/2008 12:57:44 PM	
Patient_03.ARR Batch_Register_Test	Patient_03			HG-U133A_2	1/29/2008 1:01:27 PM	
Step 3: Confirm Selection Assign Barcode to the selected Array and Save using 'Assign Barcode' button. Assign Barcode						

4. Select the check box for the array that corresponds to the array barcode.

Note: You can use the View drop-down box and Customize button to add or delete attributes for display in the Array list. For more information, see "Selecting attributes for the file list" on page 57.

5. Click Assign Barcode.

If it is successful, the result page is displayed. (Figure 166)

If the assignment was unsuccessful, the Add Barcode page is displayed with an error message.

Figure 166 Results page
Search Files By: 🛙 Array Name 👻 (Use * for wildcard) 🧧 Advanced Search 🤤
HOME DATA SAMPLES ADMINISTRATION HELP
Result Page 😢
Added @52006500461817101306401416533717 barcode successfully for the Patient_02 array of the Array file - C:\Command_Console\Data\Batch_Register_Test\Patient_02.ARR

Batch editing

Batch Edit enables you to make edits to a set of previously created Sample (ARR) files.

Note: Batch edit cannot be used to create new Sample (ARR) files. Use the various Sample Registration functions described in this chapter to create new files. Also, Batch edit cannot be used to change file or array names. Use the editing functions of the Detailed Sample Registration page to do this. See "Editing files and copying attributes" on page 110 for more information.

Using Batch Edit involves three sets of steps:

- 1. Create a batch edit file listing the files you want to edit, using the Project view, Folder, Search Results view, or use a previously created batch registration Excel file.
- 2. Edit the batch edit file, adding and changing attributes as needed.
- 3. Upload the batch edit file using the **Batch Edit Upload** function.
Creating the batch edit file

You can create a batch edit file for:

- The Sample (ARR) files in a project or folder (see "Generating a project summary" on page 86).
- Selected Sample (ARR) files (see below)

To generate a Batch Edit File for selected Sample files:

- 1. Select the Sample files from the:
 - Folder view page
 - Project view page
 - Search Results page
- 2. From the Command to Select drop-down, select the **Create Batch Edit Files** from Selected Arr files link.

The Summary page opens (Figure 167).

Search Files By: 🛙	Array Name 💌		(Use * for wildcard)	Advanced Search
IOME DATA SAMPLES A		IELP		
Generates Batch Edit f	ile 🛙			
ample (ARR) files to be in	luded in summary:			
ample (.ART) mes to be in	sidded in saminary.		_	
C:\Command_Console\Data C:\Command_Console\Data	Dr Moriarty\X_Samp Dr Moriarty\X_Samp	le_01.ARR le_02.ARR		
Command_Console\Data	Dr Moriarty\X_Samp	le_03.ARR		
Create				
Create				
Create Optional) Select additional Joload to update data in ex	templates to include sting sample(.ARR)	e in the file. These will a files.	appear as additional heade	rs. Use this with Batch Edit
Create Optional) Select additional Jpload to update data in ex	templates to include sting sample(.ARR)	e in the file. These will a files.	appear as additional heade	rs. Use this with Batch Edit
Create Optional) Select additional Ipload to update data in ex MIAME Sample Inforr	templates to include sting sample(.ARR) *	e in the file. These will a files.	appear as additional heade	rs. Use this with Batch Edit
Create Optional) Select additional Ipload to update data in ex > IMIAME Sample Inform > IMoriarty > ITestA	templates to include sting sample(.ARR) nation	e in the file. These will a files.	appear as additional heade	rs. Use this with Batch Edit
Create Optional) Select additional pload to update data in ex > IMIAME Sample Inform > IMoriarty > ITestA	templates to include sting sample(.ARR) · nation	e in the file. These will a files.	appear as additional heade	rs. Use this with Batch Edit
Create Optional) Select additional Ipload to update data in ex > IMIAME Sample Inform > Moriarty > ITestA	templates to include sting sample(.ARR) ' nation	e in the file. These will a files.	appear as additional heade	rs. Use this with Batch Edit
Create Optional) Select additional Ipload to update data in ex > IMIAME Sample Inforr > Moriarty > ITestA	templates to include sting sample(.ARR) ' nation	e in the file. These will a files.	appear as additional heade	rs. Use this with Batch Edit
Create Optional) Select additional Ipload to update data in ex > MIAME Sample Inforr > Moriarty > TestA	templates to include sting sample(.ARR) ' nation	e in the file. These will a files.	appear as additional heade	rs. Use this with Batch Edit

A list of Sample (ARR) files that will be in the summary appears.

- 3. Select a template to be used in editing (optional).
- 4. Click Create.



The Excel program displays the created workbook (Figure 168), which you can edit and save on your computer.

You can also edit a previously created Batch Registration file, adding attributes as needed. See "Entering values in the batch registration file" on page 126 for more information about editing Batch Registration files.

Editing the batch edit file

The downloaded Excel workbook has three worksheets:

- Samples worksheet
- General info worksheet (do not edit)
- Template Info worksheet (do not edit)

Figure 168 Batch Ed	dit Excel W	/orkbook,	Samples	works	heet			
	0	D	E	F		L	1	
1 Sample File Path	Sample File Name	Array Name	Probe Array Type	Barcode	gender:TestA:SingleSelect:Required	age:TestA:Number:Required	tissue type:TestA:Text	-^
2 C:\Command Console\Data\Dr Moriarty	X Sample 01	X Sample 01 A	HG-U133A		M	34	Brain	
3 C:\Command Console\Data\Dr Moriarty	X Sample 01	X Sample 01 B	HG-U133B		M	34	Brain	
4 C:\Command Console\Data\Dr Moriarty	X Sample 02	X Sample 02 A	HG-U133A		F	36	Liver	
5 C:\Command_Console\Data\Dr Moriarty	X_Sample_02	X_Sample_02_B	HG-U133B		F	35	Liver	
6 C:\Command_Console\Data\Dr Moriarty	X_Sample_03	X_Sample_03_A	HG-U133A		M	44	Kidney	
7 C:\Command Console\Data\Dr Moriarty	X Sample 03	X Sample 03 B	HG-U133B		M	44	Kidney	
8								
9								
10								
11								Π_

The header row of the Samples worksheet includes special properties that define the file and the physical array:

Sample File Path	The path to where the Sample file is located.
Sample File Name	Unique identifier for the Sample file.
Array Name	Name assigned to the array during registration.
Probe Array Type	Part number for the array(s).
Barcode	Barcode on the array(s)
Attributes	Additional information about the sample and experiment that you can use to interpret your results.

The General Information Worksheet and the Template Info Worksheet (both marked **Do Not Edit**) contain information used by GCC in processing the data in the workbook.

Make the changes in the summary file to edit the files. You can:

- Enter attribute values
- Add user attributes with values
- Delete attributes from the Sample (ARR) file

Note: You can not make changes to file names or array names using this feature. Do not make changes to file names in the downloaded file.

The following items in the workbook must not be edited.

Sample File Path The Path and Sample (ARR) file name.

Array Name Array name assigned to the files.

Note: If you delete a the entire column for a template attribute, including the header, then an error will be generated. In order to remove attribute values from a sample file, users need to leave the header intact and remove the attribute values from the column

The first row of the workbook defines the data to be edited. Each additional row contains the information for one Sample (ARR) file.

Multiple arrays for a single sample (ARR) file

If you have multiple arrays assigned to a single sample file, each array is on a separate line of the worksheet.

Figure 169 Multiple arrays			
	, v		
Sample File Path	Sample File Name	Array Name	Probe Array Type
C:\Command_Console\Data\Dr Moriarty	Dr_Smith_01	Dr_Smith_01_(HG-U133A_2)	HG-U133A_2
C:\Command_Console\Data\Dr Moriarty	Dr_Smith_01	Dr_Smith_01_(HG-U133A)	HG-U133A
lata i fa i tip tip te tri			110 11000 0

You cannot enter different attributes values for the same attributes for arrays associated with the same Sample (ARR) file.

Editing the barcode

You can only add a barcode to a Sample (ARR) file that does not already have one. You cannot edit a barcode that is already assigned to the Sample (ARR) file.

- If you assign a barcode to a Sample file, a warning message appears if the probe array type specified in the barcode does not match the probe array type previously assigned to the array.
- You can assign a custom barcode to a Sample file.

Editing attributes

Enter the values for the attributes in the appropriate columns. See "Attributes" on page 129 for more information.

After editing the batch edit file, you need to upload the data into GCC.

Uploading the edited file

1. From the Samples menu, select **Batch Edit Upload**.

The Batch Edit Attribute page opens. (Figure 170)

k	\sim	*		ŝ.	Ī
		Ľ	Ľ	5	
		U	88	2	
				1	
		2	-	4	

Figure 170	Batch Edit Attribute page
Search I HOME DATA	Files By: 🛛 Array Name 💌 (Use * for wildcard) 🎴 Advanced Search SAMPLES ADMINISTRATION HELP
Batch Edit A	ttribute 🛙
Start > Confin	m • Finish
• Create nev • Create nev • Change fil	ws you to make edits to a set of previously created Sample (.ARR) files. Batch edit cannot be used to: w Sample (.ARR) files e or array names
Step 1: Create	Excel Spreadsheet
Create a sprea	dsheet using Folder View, Project View or Search Results Summary; or use a batch registration spreadsheet.
Step 2: Edit Ex	cel Spreadsheet 🔟
The first row of (.ARR) file. Add	f the spreadsheet defines the data to be edited. Each additional row contains the information for one Sample ditional columns can be added at any time to the spreadsheet to add attributes.
Step 3: Upload	l Spreadsheet
Select the edite	ed spreadsheet (.XLS format). Browse
Allow Custo	m Barcodes
Upload	

- 2. Enter the file path and name in the box; or
 - a. Click **Browse** to open the Choose File window.
 - b. Select the Batch Registration or Batch Edit file and click **Open**.

The file and its path is displayed in the box.

3. In the Upload Spreadsheet section, click on Upload.

If there is a problem with the workbook, the Confirm Batch Edit Sample Files produces a warning, as shown in Figure 171.

Figure 171 Error notice
Search Files By: Image: Ima
Confirm Batch Edit Sample Files 💷
Start > Confirm > Finish
Errors:
Unable to consolidate the sample at the row 4. The column "age:TestA:Number:Required" has different value or type for the same sample attribute of the sample file "C:\Command_Console\Data\Dr Moriarty\X_Sample_02.ARR".
If you wish to continue editing, click the Next button and only the records with no errors will be edited. You may cancel the operation by clicking the Cancel button.
Cancel

If there are no issues, the Confirm Batch Edit page opens. (Figure 172)

Figure 172 Confirm Batch Edit
Search Files By: 🛛 Array Name 👻 (Use * for wildcard) 🧧 Advanced Search 🎈
HOME DATA SAMPLES ADMINISTRATION HELP
Confirm Batch Edit Sample Files 💷
Start > Confirm > Finish
Batch edit file has been loaded without any errors. Do you want to save samples?
Cancel Save

4. Click **Save** to edit the valid records.

A batch edit is complete message appears.



Controlling the fluidics station

Hybridizing and processing the array is the next step after sample registration in the recommended array processing workflow. (Figure 173)



The Fluidics Station 450 is used to hybridize, wash, and stain the GeneChip probe arrays (called arrays in this manual). The FS450 can independently process an array using a different fluidics protocol in each of four different modules.



- Disconnect the power cord of Fluidics Station before replacing fuses.
- Use a surge protector on the power line to the fluidics station.
- The fluidics station should be positioned on a sturdy, level bench away from extremes in temperature and away from moving air.

Note: You must have the required fluidics protocols installed before using the FS450. For more information, see "Installing and updating protocols" on page 172.

The GCC Fluidics Control software is used to control the FS450 Fluidics Station. A workstation with GCC Fluidics Control software and a Sealevel card installed can control up to eight different fluidics stations.

Note: Before you use the fluidics station, check the fluidics station configuration and prime the fluidics station with appropriate buffer. For more information, read this chapter.

This chapter describes how to use the GCC Fluidics Control software in the following sections:

- "GCC fluidics control software"
- "Running protocols" on page 155
- "Filtering the sample file list" on page 166
- "Adding a label to a station and modules" on page 171
- "Installing and updating protocols" on page 172
- "Editing protocols" on page 175

Refer to the *GeneChip Fluidics Station User's Guide* for a description of the instrument itself.

You can set things up to provide email notification when protocols are complete or problems develop. See Appendix E, "Notification e-mails" on page 367 for more information.

GCC fluidics control software

The GCC Fluidics Control software is used to control the FS450 Fluidics Station. The software is introduced in the following sections:

- "Starting", below
- "Master controls" on page 153
- "Station controls" on page 153
- "Status window" on page 155

Starting

1. In the GCC Launcher, click the GCC Fluidics Control Icon; or Click Start \rightarrow Thermo Fisher Scientific \rightarrow GCC Fluidics Control... The GCC Fluidics Control window opens (Figure 174).

-igure 174 GUUF	luidics Control Window, Maste	er controis	
Menu bar		0	
Tool bar	Run All Run Str. Filters Refresh Settings Edit Email Info Master Station 1 ID:	Help	
Master/Station	Step 1: Select Probe Array Type Probe Array Type:	Check/Uncheck All Stations and Modules	
	Step 2: Select Protocol	T Station 1 ID:	C Station 5
	List All Protocols	Module 1 Module 2 Module 3 Module 4	Module 1 Module 2 Module 3 Module 4
	List Compatible Protocols Only GeneChip IVI Labeling Kit GeneChip HWS Kit	E Station 2	E Station 6
	C List Custom Protocols Only	T Module 1 T Module 2 T Module 3 T Module 4	Module 1 Module 2 Module 3 Module 4
	C List Maintenance Protocols Only	F Station 3	E Station 7
	Protocol:	🗖 Module 1 🗖 Module 2 🗖 Module 3 🗖 Module 4	Module 1 🗖 Module 2 🗖 Module 3 🗖 Module 4
	Step 3: Copy to selected modules/stations		
	Copy to Selected Modules	Module 1 Module 2 Module 3 Module 4	Module 1 Module 2 Module 3 Module 4
	Station Module Array Name Probe Array Tupe Barcode ID User	Protocol Date Time Durrent Stage Trime / D	vole Temp Time Remaining
.			
Status window			
Status bar			

Components of the GCC Fluidics Control window:

- Menu bar: Provides access to Fluidics Control functions.
- Tool bar: Provides quick access to frequently used functions.
- Master/Station controls: Click the tabs to switch between:
 - "Master controls" (see below): Use to select a single protocol to run on multiple stations and/or modules.
 - "Station controls": Use to select different protocols to run on different modules in a station.
- Status window: Displays list of arrays in process with information on their status. See "Status window" on page 155.
- **Status bar**: Displays information about the status of the Fluidics station and the fluidics run in progress.

Hiding or displaying the tool bar

1. From the View menu, select **Toolbar** \rightarrow **Standard Toolbar**.

Adding text labels to the toolbar buttons

1. From the View menu, select **Toolbar** \rightarrow **Text Labels**.

Hiding or displaying the status bar

1. From the View menu, select Status Bar.

Master controls

The Master controls (Figure 175) enable you to select a single protocol to run on any or all stations and modules attached controlled by the workstation.

Protocol Selection	Station and Module Selection
r Station 1 ID:	
robe Array Type vobe Array Type	Check/Uncheck All Stations and Modules
rep 2: Select Protocol	Station 1 ID: Module 1 Module 2 Module 3 Module 4
List Compatible Protocols Only GeneChip IVT Labeling Kit GeneChip HWS Kit List Custom Protocols Only	Image: Station 2 Image: Station 6 Image: Module 1 Image: Module 3 Image: Module 4 Image: Module 1 Image: Module 3 Image: Module 4
C List Maintenance Protocols Only Protocol:	Station 3 Module 1 Module 2 Module 3 Module 4 Module 1 Module 4 Mod

The Master controls are used for:

- "Running a priming or maintenance protocol on multiple stations and modules" on page 156.
- "Running a fluidics protocol on multiple stations" on page 157

Station controls

The Station controls enable you to select arrays and protocols for each module of a selected station (Figure 176). The controls enable you to:

- Select a particular array for processing using the following parameters:
 - Sample File Name
 - Array Name
 - Probe Array type
- Select a specific protocol for the array.

Figure 176 GCC Fluidics	Control window, Station co	ontrols	
Master Station 1 ID:			
Module 1 ID:	Module 2 ID:	Module 3 ID:	Module 4 ID:
Barcode:	Barcode:	Barcode:	Barcode:
Sample File Name:	Sample File Name:	Sample File Name:	Sample File Name:
•	•	_	_
Array Name:	Array Name:	Array Name:	Array Name:
V		×	_
Probe Array Type:	Probe Array Type:	Probe Array Type:	Probe Array Type:
•	•	T	•
Select Protocol	Select Protocol	Select Protocol	Select Protocol
C All C Compatible C Custom C Maintenance	All C Compatible C Custom C Maintenance	C All C Compatible C Custom C Maintenance	
🔽 GeneChip IVT Labeling Kit 📃 GeneChip HWS Kit	🔲 GeneChip IVT Labeling Kit 📄 GeneChip HWS Kit	🔲 GeneChip IVT Labeling Kit 🔲 GeneChip HWS Kit	🔽 GeneChip IVT Labeling Kit 🔲 GeneChip HWS Kit
Protocol:	Protocol:	Protocol:	Protocol:
	•	-	
Step:	Step:	Step:	Step:
•	· ·		•
Run	Run	Run	Run

Each module has its own set of controls. (Figure 177)

Figure 177 Module controls
Module 2 ID:
Barcode:
Sample File Name:
·
Array Name:
Probe Array Type:
Select Protocol
🔲 🔲 GeneChip IVT Labeling Kit 🔲 GeneChip HWS Kit
Protocol:
_
Step:
_
Run

The use of the module controls is described in "Running fluidics on individual stations" on page 160.

GeneChip[™] Command Console[™] (GCC) User Guide



Status window

	Figure 178 Status window												
	Station	Module	Array Name	Probe Array Type	Barcode ID	User	Protocol	Date Time	Current Stage	Time / Cycle	Temp	Time Remaining	
Ш	1	2	October_11_02_HG-U133A_Rep	2 HG-U133A.Expression			FlexFS450_0001	2006-10-11 14:26:00	Running	3:52	21.0	1:19:01	
Ш	1	1	October_11_02_HG-U133A_Rep	1 HG-U133A.Expression			FS450_0001	2006-10-11 14:26:00	Running	3:48	20.0	1:18:52	
Ш													
Ш													
Ш													
JĽ													

The Status Window (Figure 178) displays:

- Station: Fluidics station in operation.
- Module: Module in operation.
- Array Name: Name assigned to the array.
- Probe Array Type
 - Barcode ID: The last five digits of the probe array barcode.
 - User: Person who created the Sample file.
 - Protocol: Protocol used for the fluidics run.
 - **Date Time**: Current data and time when a protocol is running, or data and time when it was complete.
 - Current Stage: Fluidics protocol stage currently running.
 - Time/Cycle: Amount of time left for current stage or wash cycle number (e.g. 2 of 4).
 - **Temp**: Temperature used for current stage.
 - **Time Remaining**: Total time remaining for protocol.

Running protocols

You have several different options for selecting and running protocols with GCC Fluidics Control, depending upon:

- The type of protocol you want to run.
- Whether you want to run it on multiple stations.
- Whether you want to select different protocols for different modules in a station.

This section describes how to select and run protocols using GCC Fluidics Control:

- "Running a priming or maintenance protocol on multiple stations and modules" on page 156
- "Running a fluidics protocol on multiple stations" on page 157
- "Running fluidics on individual stations" on page 160
- "Resuming a fluidics protocol" on page 164
- "Bypassing steps in a fluidics protocol" on page 165

Running a priming or maintenance protocol on multiple stations and modules

Priming fills the fluidics station lines with wash buffers and deionized water. The GeneChip Fluidics Station must be primed before it can be used to run assay protocols. Prime the fluidics station when:

- The fluidics station is first turned on.
- A wash solution is changed.
- The fluidics station is to be used again after a shutdown has been performed.
- A module LCD window informs you that the module is not primed.

This section explains how to run priming or maintenance protocols on multiple stations and modules.

Priming the fludics station

1. Start the GCC Fluidics Control Software.

See "GCC fluidics control software" on page 151.

The software opens with the Master controls displayed.

2. In the Select Protocols section of the Master controls, select List Maintenance Protocols Only.

Figure 179 Selecting the Prime protocol							
Select to list maintenance protocols Step 3: Copy to selected modules/stations Copy to Selected Modules	Then select Prime_450 from the list						

3. Select *Prime_450* from the **Protocol** drop-down list; or

Select the maintenance protocol you want to run.

4. Select the modules to be primed (Figure 180).

Figure 180 Selecting the stations and modules for priming

	Theck/Uncheck All :	Stations and Modu	les				
Station 1 ID:	Module 2	Module 3	Module 4	C Station 5	Module 2	Module 3	Module 4
Station 2 Module 1	Module 2	Module 3	Module 4	Station 6	Module 2	Module 3	Module 4
☐ Station 3				Station 7			
Module 1	Module 2	Module 3	Module 4	Module 1	Module 2	Module 3	Module 4
Module 1	Module 2	Module 3	Module 4	Module 1	Module 2	Module 3	Module 4

You can:

- Select individual check boxes for each module.
- Click the Station ID check box to select all modules for a particular station.
- Click **Check/Uncheck all Stations and Modules** to select/deselect every station and module.
- 5. Click Copy to Selected Modules.
- 6. The selected protocol (Prime_450) is applied to the selected stations and modules.
- 7. Fill the intake buffer reservoirs A and B with the appropriate priming buffer. (Refer to the appropriate GeneChip probe array package insert).
- 8. Empty the waste bottle and fill the water reservoir with deionized water.
- 9. Load an empty, standard 1.5 mL microcentrifuge tube in the sample holder of each module to be primed.
- 10. Click the Run All button (); or

Select Start \rightarrow Run All Modules Selected on Master Page.

11. Follow the prompts in the **Status window** (also shown in the module LCD window).

The Status window and the module LCD window display the status of the procedure. The fluidics station is ready to use when priming is completed and **Priming done, Ready** appears in the module LCD window.

Running a fluidics protocol on multiple stations

You can run a selected protocol on any or all modules in the Fluidics stations attached to the workstation using the Master controls.

Selecting and running a fluidics protocol for a set of probe arrays

1. Start the GCC Fluidics Control Software.

See "GCC fluidics control software" on page 151.

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The software opens with the Master controls displayed (Figure 181).

Figure 181 Master controls								
Master Station 1 ID: Step 1: Select Probe Array Type Probe Array Type:	Check/Uncheck All Stations and Modules							
Step 2: Select Protocol	Station 1 ID: Module 1 Module 2 Module 3 Module 4	Station 5 Module 1 Module 2 Module 3 Module 4						
C List Compatible Protocols Only GeneChip IVT Labeling Kit GeneChip HWS Kit C List Custom Protocols Only	Station 2 Module 1 Module 2 Module 3 Module 4	Station 6 Module 1 Module 2 Module 3 Module 4						
C List Maintenance Protocols Only Protocol:	Station 3 Module 1 Module 2 Module 3 Module 4	Station 7 Module 1 Module 2 Module 3 Module 4						
Step 3: Copy to selected modules/stations Copy to Selected Modules	Station 4 Module 1 Module 2 Module 3 Module 4	Station 8 Module 1 Module 2 Module 3 Module 4						

2. Select the array type from the Probe Array Type list. (Figure 182)

Figure 182 Selecting probe array type							
Step 1: Select Probe A	тау Туре						
Probe Array Type:	7GComplex5umGeno.Mapping	- -					
Step 2: Select Protocol	Hg.sxpression ATH1-121501.Expression ax26087_a_ref_dir.Mapping Barley1.Expression						
List All Protoco	Bovine.Expression Citrus.Expression Citrus. SNP.Manning						
C List Compatible	DCNtag1Qr510989.Resequencing E coli 2.Expression	~					

IMPORTANT! The protocol that is displayed in the Protocol drop-down box after selecting the probe array type may or may not be the correct protocol for the array, depending upon the type of analysis being performed. To make sure the correct protocol is selected, follow the steps below.

3. Limit the protocols listed by selecting from the different options (Figure 183).

Figure 183 Selecting options to filter the list of pr	rotocols
Step 2: Select Protocol List All Protocols List Compatible Protocols Only GeneChip IVT Labeling Kit List Custom Protocols Only List Maintenance Protocols Only Protocol: Midi euk2v3_450	Select the options for filtering protocols

To limit the protocols listed:

- c. Select one of the following buttons:
 - List All Protocols
 - List Compatible Protocols Only (displays only protocols that can be used with the selected labeling kit):

Select the appropriate check box:

- -GeneChip IVT Labeling Kit
- -GeneChip HWS Labeling Kit
- List Custom Protocols Only (displays only protocols that have been edited or provided by the user)
- List Maintenance Protocols Only (displays only maintenance protocols)

Only the protocols that meet the selected requirements are displayed in the Protocol drop-down list.

4. Select the protocol from the **Protocol** drop-down list (Figure 184).

Figure 184 Selecting protocols from the list								
Step 2: Select Protocol C List All Protocols G List Compatible Protocols Only G GeneChip IVT Labeling Kit C List Custom Protocols Only C List Maintenance Protocols Only Protocol: Midi_euk2v3_450 Midi_euk2v3_450	Select the protocol from the drop-down list							

IMPORTANT! The protocol that is displayed in the Protocol drop-down box after selecting the probe array type may or may not be the correct protocol for the array, depending upon the type of analysis being performed. To make sure the correct protocol is selected, select the correct options for filtering the protocol list as described above.

- 5. Select the modules to be run by:
 - Selecting individual check boxes for each module.

- Clicking the Station ID check box to select all modules for a particular station.
- Clicking **Check/Uncheck all Stations and Modules** to select/deselect every station and module.

Figure 185	Selecting s	stations an	d Modules					
	Check/Uncheck All	Stations and Modu	les					
Station 1 ID:					🔲 Station 5			
Module 1	Module 2	Module 3	Module 4		Module 1	Module 2	🗖 Module 3	Module 4
🗖 Station 2					🔲 Station 6			
Module 1	🔲 Module 2	🔲 Module 3	🗖 Module 4		🔲 Module 1	Module 2	🗖 Module 3	Module 4
Station 3					🗖 Station 7			
Module 1	Module 2	Module 3	Module 4		Module 1	Module 2	Module 3	Module 4
				_				
Station 4					🗖 Station 8			
Module 1	🔲 Module 2	🗖 Module 3	🗖 Module 4		Module 1	Module 2	🔲 Module 3	Module 4

6. Click Copy to Selected Modules.

The selected protocol is applied to the selected stations and modules.

- 7. Fill the intake buffer reservoirs A and B with the appropriate solutions (Refer to the appropriate GeneChip probe array package insert).
- 8. Empty the waste bottle and fill the water reservoir with deionized water.
- 9. Click the Run All button 💽 💓 ; o

Select Start \rightarrow Run All Modules Selected on Master Page.

The Status window and the module LCD window display the status of the procedure.

10. After the protocol is finished, remove the probe array and inspect the probe array window for air bubbles.

If air bubbles are present, reinsert the probe array into the fluidics station to automatically drain and refill the probe array with the last wash buffer used. (Refer to the appropriate GeneChip probe array package insert.) If no bubbles are present, the probe array is ready to be scanned.

Running fluidics on individual stations

You can also select a particular fluidics protocol on an individual station and module.

Selecting and running a fluidics protocol on an individual station and module

1. Start the GCC Fluidics Control Software.

See "GCC fluidics control software" on page 151.

The software opens with the Master controls displayed.

2. Click the tab for the station you want to use (Figure 186).

Figure 186 Tabs for Master and Station controls							
File Edit View Start Help							
C Image: Section of the section of t							
Master Station 1 ID:							

The Station controls displays the module controls for the selected station. Each module control has the same functions (Figure 187).

Figure 187 Module control
Module 2 ID:
Barcode:
Sample File Name:
•
Array Name:
Probe Array Type:
•
Select Protocol
• All C Compatible C Custom C Maintenance
🔲 GeneChip IVT Labeling Kit 🔲 GeneChip HWS Kit
Protocol:
_
Step:
Run

- 3. Click the Refresh button to refresh the list of Sample files.
- 4. Click in the Barcode box and enter the barcode using the keyboard; or Scan the barcode with an external barcode reader.
- 5. Press the Tab key.

The following items are selected automatically if the barcode is valid:

- Sample File name: Sample File with which the barcode is associated.
- Array Name: Array name with which the barcode is associated.
- Probe Array Type: Probe array type with which the barcode is associated.

Figure 188 Barcode entered, Sample File name, Array Name, and Probe Array type automatically selected							
Macter Station 1 ID:							
Module 1 ID: Barcode:							
@52006500461817101308401416533702							
Sample File Name:							
Pre_Register_02							
Array Name:							
Pre_Register_02_(HG-U133A_2)							
Probe Array Type:							
HG-U133A_2.Expression							
Select Protocol							
C All C Compatible C Custom C Maintenance							
GeneChip IVT Labeling Kit GeneChip HWS Kit Protocol:							
Midi_euk2v3_450							
Step:							
1 - Wash A1							
Run							

If you enter a valid barcode or specify the array name by other means, the fluidics protocol information is kept with the Audit file for the array.

You can also:

- Select a Sample file without entering the barcode. In this case, if the Sample file has more than one array associated with it, you will need to select the proper array from the Array Name list.
- Specify a protocol without specifying a Sample file or array. In this case, the fluidics protocol information is kept in an audit file that does not link to a particular Sample file.

Note: You can use the Filter dialog box to limit the Sample (ARR) files displayed by various properties. See "Filtering the sample file list" on page 166.

IMPORTANT! The protocol that is displayed in the Protocol drop-down box after entering a barcode or selecting a sample name or probe array type may or may not be the correct protocol for the array, depending upon the type of analysis being performed. To make sure the correct protocol is selected, follow the steps below.

6. Set the options to filter the fluidics protocol selections.

Figure 189 Selecting options for protocol selection								
Select Protocol C All C Compatible C Custom C Maintenance G GeneChip IVT Labeling Kit GeneChip HWS Kit Protocol: Mid_euk2v3_450	Select the options for filtering protocols							

To limit the protocols listed select one of the following buttons:

- All (lists all protocols available on your computer)
- Compatible (displays only protocols that can be used with the selected labeling kit):

Select the appropriate check box:

- GeneChip IVT Labeling Kit
- GeneChip HWS Labeling Kit
- Custom (displays only protocols that have been edited or provided by the user)
- Maintenance (displays only maintenance protocols)

Only the protocols that meet the selected requirements are displayed.

7. Select the fluidics protocol from the Protocol list.

Figure 190 Selecting the protocol	
Select Protocol C All Compatible C Custom C Maintenance G GeneChip IVT Labeling Kit GeneChip HWS Kit Protocol: Midi_euk2v3_450 Midi_euk2v3_450 Midi_euk2v3_450	Select the protocol from the list

IMPORTANT! The protocol that is displayed in the Protocol drop-down box after entering a barcode or selecting a sample name or probe array type may or may not be the correct protocol for the array, depending upon the type of analysis being performed. To make sure the correct protocol is selected, select the correct options for filtering the protocol list as described above.

8. Click Run to start the protocol on the selected module; or

From the Start menu, select Run All Modules on Current Station; or

Click the Run All Modules on Current Station button

9. Load the probe array and sample vial holder containing the appropriate solution in each active module.

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Sensors in the fluidics station detect when the probe array and sample vial holder have been loaded. The process will proceed automatically from this point, although some protocols may require removal and substitution of the sample vial and solution. The Fluidics Status window displays the status of the procedure (see "Status window" on page 155).

Figure 191 Fluidics Control window, protocol running			
File Edit View Start Help			
Run All Run Stn Filters Refresh Settings Edit	Email Info Help		
Master Station 1 ID:			
Module 1 ID:	Module 2 ID:	Module 3 ID:	Module 4 ID:
Barcode:	Barcode:	Barcode:	Barcode:
@52006500461817101308401416533702			
Sample File Name:	Sample File Name:	Sample File Name:	Sample File Name:
Pre_Register_02	Dr_Smith_01	_	_
Array Name:	Array Name:	Array Name:	Array Name:
Pre_Register_02_(HG-U133A_2)	Dr_Smith_01_(HG-U133A_2)		
Probe Array Type:	Probe Array Type:	Probe Array Type:	Probe Array Type:
HG-U133A_2.Expression	HG-U133A_2.Expression		· · · · · · · · · · · · · · · · · · ·
Select Protocol	Select Protocol	Select Protocol	Select Protocol
C Al C Compatible C Custom C Maintenance	C All C Compatible C Custom C Maintenance	C All C Compatible C Custom C Maintenance	
🔽 GeneChip IVT Labeling Kit 🛛 🗖 GeneChip HWS Kit	🔽 GeneChip IVT Labeling KR: 🗧 GeneChip IVT S KR: 🔲 🔽 GeneChip IVT Labeling KR: 🔽 GeneChip IVT Labeling KR: 🔲 GeneChip IVT Labeling KR: 🗐 GeneChip IVT Labeling KR:		
Protocol:	Protocol:	Protocol:	Protocol:
Midi_euk2v3_450	Midi_euk2v3_450	-	
Step:	Step:	Step:	Step:
1 - Wash A1	1 - Wash A1	_	_
Stop	Stop	Run	Run
Station Module Array Name Probe Array Type	Barcode ID User Protocol Date Tir	ne Current Stage Time / Cycle	Temp Time Remaining
1 1 Pre_Register_0 HG-U133A_2.Expressi 1 2 Dr. Swith 01.0 HG-U133A_2.F.	: 33702 rallso Midi_euk2v3_450 2008-02	-22 15:56:00 Running	0:59:58
2 Di_Shikr_Dr_(r Ho-01334_2/Express)	ransu mujeuk.2v5_430 2008-02	raa rataataa ataliing	
1			
▲			•

- 10. Repeat as necessary for other modules in the fluidics station(s).
- 11. After the protocol is finished, remove the probe array and inspect the probe array window for air bubbles.

If air bubbles are present, reinsert the probe array into the fluidics station to automatically drain and refill the probe array with the last wash buffer used. (Refer to the appropriate GeneChip probe array package insert.) If no bubbles are present, the probe array is ready to be scanned.

Resuming a fluidics protocol

GCC tracks the progress of a fluidics protocol run. If the protocol stops before completion, it can be resumed at the point where it was interrupted.

Note: The resume feature is only available for fluidics protocols that display multiple steps in the **Step** drop-down list of the Fluidics Station dialog box and that have failed. If you exit GCC Fluidics Control while a fluidics protocol is running, the resume feature will be unavailable upon startup of the software.

1. Click **Resume** in the Modules controls.

The selected protocol is started in modules one through four of the fluidics station.

Bypassing steps in a fluidics protocol

Some multi-step fluidics protocols can be started at any step, so that part of a protocol can be bypassed.

Note: The bypass function is only available for fluidics protocols that display multiple steps in the **Step** drop-down list of the Fluidics Station dialog box.

Bypassing steps

- 1. Select an array and protocol as described in "Running a fluidics protocol on multiple stations" on page 157.
- 2. Select the desired beginning step from the Step drop-down list (Figure 192).

Figure 192Bypassing protocolsteps 1, 2, and 3		
Master Station 1 ID:		
Module 1 ID:		
Barcode:		
@51059900413526052906400976113289		
Sample File Name:		
@51059900413526052906400976113289		
Array Name:		
@51059900413526052906400976113289		
Probe Array Type:		
Test3.Expression		
Select Protocol		
C All C Compatible C Custom C Maintenance		
GeneChip IVT Labeling Kit 🔲 GeneChip HWS Kit		
Protocol:		
Micro_1v1_450		
Step:		
1 - Wash A1		
1 - Wash A1		
3 - Stain 1		
4 - Wash A2		

3. Click Run to start the fluidics protocol at the selected step.



Filtering the sample file list

When first opened, the Sample file list in the module control displays all the Sample files available in GCC. (Figure 193)

Figure 193 Station controls with unfiltered Sample File list
Master Station 1 ID:
Module 1 ID:
Barcode:
Sample File Name:
Moriarty_05
@51059900413526052906400976113289 @52006500461817101308401416533701 @52006500461817101308401416533702 @52006500461817101308401416533703 Dr_Smith_01 Dr_Smith_02 Dr_Smith_03 Moriarty_04
C All C Compatible C Custom C Maintenance GeneChip IVT Labeling Kit GeneChip HWS Kit Protocol:
EukGE-WS2v4_450
Step:
1 - Wash A1
Run

You can use the Filter dialog box to limit the types of files displayed in the Sample File list.

Note: The Filter dialog box can also be used in the GCC Scan Control in Manual mode.

Using the Filter dialog box

1. Click the Filters button T; or

From the Edit menu, select **Filters...**.

The Filters dialog box opens. (Figure 194)

Figure 194 Filters	Figure 194 Filters dialog box		
Date From Friday ,	May 11, 2007 💌 🗖 To Wednesday, June 27, 2007 💌		
Selected Project Names:			
Selected Probe Array Types: [All Arrays]			
Attribute Attribut 1 IJSERI;Assay Type 2 IJSERI;Automati 3 IJSERI;Comments 4 IJSERI;Experime 5 IJSERI;Food Type 6 IJSERI;Probe Arr 7 IJSERI;Reagent 8 IJSERI;Sample D	e value (Select to Edit)		
Include Scanned Arrays	Array Name Wildcard Array Name		
	OK Cancel		

The Filters dialog box enables you to filter the displayed Sample files by:

- Date: Files created on a date or range of dates.
- Selected Project Names: Files associated with a particular project.
- Selected Probe Array Types: Files for a specific probe array model.
- **Template attributes and values**: Files associated with a particular attribute value.
- Array Scan status: Files for arrays that have already been scanned.
- Array Name wildcard: Array names with a specified text string in their file name.
- 2. Select a date or range of dates for file creation:
 - a. Select the From check box.
 - b. Click the arrow at the date (displays the current date).
 - A calendar for the current month appears. (Figure 195)



- c. Select a date for the start of the range. You can move from month to month by clicking the < and > buttons.
 - If you only select one date, the filter will display only the files created on that date.

To select a range of dates:

- d. Select the **To** check box.
- e. Select a date for the end of the range.
- 3. Select projects from the Project Name drop-down list:
 - a. Click the down button in the Project Name list.

A list of the projects available in GCC on this computer is displayed. (Figure 196)

	Figure 196	Displaying Project List
	[All Projects]	I
	[All Projects]	W
	Build37EU133	a
	Data	
-	Default	-
e	Flat	-
	For_Richard	
	GCOS 1.3	
	✓Plus2	J.
	Rec_Test	
	test	

b. Select the check boxes next to the projects you want displayed in the filtered list.

Note: For more information about creating and using projects, see "Projects" on page 34.

- 4. Select Probe Array Types:
 - a. Click on the down arrow in the Selected Probe Array Types list.

A list of the available probe array types is displayed. (Figure 197)

In some cases there may be multiple array models under the same header. in these cases you can click the + button to display the additional probe arrays.

Figure 197 Displa	aying array types
Selected Probe Array Types: User Attribute User / 1 IUSERI:Assay Type 2 IUSERI:Automati 3 IUSERI:Comment 4 IUSERI:Experime 5 IUSERI:Sample D 6 IUSERI:Sample D 7 IUSERI:Sample P 8 IUSERI:Sample T	[All Arrays]
- Include Scanned Arrays	Mapping50K_Hind240 Array Name

- b. Select the check boxes next to the probe array types you want displayed in the filtered list.
- 5. Select template attributes and enter values:
 - a. Locate the attribute you want to filter by.

Attributes are listed in the format: |Template Name|: Attribute Name.

User attributes are listed as: |USER|: Attribute Name. See "User attributes" on page 25 for more information about user attributes.

b. Click in the check box next to the attribute name. (Figure 198)

Figure 198	Selecting an attribute	
r		
User Attribute	User Attribute value (Select to Edit)	
7 (USER):Sample P		
8 USER :Sample T		
9 USER :Sample U		
🗹 10 Default:Gender		
🔲 11 Default:Height		
12 Default:Sample		_
13 Default:Weight		
14 New_Template		~

c. Click in the User Value column next to the attribute and enter a value (Figure 199).

You can use the * symbol as a wildcard in the User Value column.

6

Figure 199	Entering an attribute value	
		
User Attribute	User Attribute value (Select to Edit)	<u>~</u>
7 IUSERI:Sample P 8 IUSERI:Sample J 9 IUSERI:Sample J 10 Default:Gender 11 Default:Gender 12 Default:Sample 13 Default:Weight 14 New_Template]

Note: The Sample Attribute Conversion function may impact your selection of templates and attributes. For more information, see ""Sample attributes conversion" on page 115.

6. Deselect the **Include Scanned arrays** check box to exclude arrays that have already been scanned; or

Select the check box to display all arrays, including scanned arrays.

7. Enter a text string (used in different array names) in the Array Name wildcard text box, using the * symbol as a wild card.

For example, if you have used the barcode as an array name, entering "@*" will display all array with filenames using a barcode.

8. Click **OK**.

The filtered Sample file list is displayed in the module controls. (Figure 200) A Filters Applied notice appears above the list.

Adding a label to a station and modules

You can add a label to a station or module in the GCC Fluidics Control software. The labels can be useful when you are using more than one Fluidics station. The labels appear in the Fluidics Control software and will be used in status e-mails and in the Audit file (see Appendix E, "Notification e-mails" on page 367).

1. Click the Settings button (S); or

From the Edit menu, select Station Settings...

The Fluidics Options dialog box opens (Figure 201).

Figure 201 Fluidics Options dialog box
Fluidics
Station Number: 1 💌
Station ID:
Module 1 ID: Module 2 ID:
Module 3 ID: Module 4 ID:
🔽 Warn if Protocol Selected is not Compatible
Scanner
Scanner ID:
OK Cancel

- 2. Set the number of Fluidics stations installed in the Fluidics Stations Installed box.
- 3. Select the number of the station you want to label from the Station Number list.
- 4. Enter a label for the station in the Station ID box.
- 5. Enter labels for the modules in the Module ID boxes.
- 6. Click **OK**.
- 7. The Restart Notice appears (Figure 202).

Figure 202 Restart Notice		
⚠	The Fluidics Control software must be closed and restarted so that these changes can take effect. Make sure that all protocols have finished before closing the application.	
	ОК	

- 8. Click OK to close the Restart Notice.
- 9. Shut down and restart GCC Fluidics Control.

The labels are used in the station controls. (Figure 203)

Figure 203 Station Controls with labels					
File Edit View Start Help	Email Info Help				
Module 1 ID: First Module Barcode: I Sample File Name: Filters applied	Module 2 ID: Second Module Barcode: Sample File Name: Filters applied	Module 3 ID: Third Module Barcode: Sample File Name: Filters applied	Module 4 ID: Fourth Module Barcode: Sample File Name: Filters applied		
Array Name:	Array Name:	Array Name:	Array Name:		
Select Protocol ⊂ All © Compatible ⊂ Custom ⊂ Maintenance ⊽ GeneChip IVT Labeling Kit □ GeneChip HWS Kit Protocol	Select Protocol C All C Compatible C Custom C Maintenance G GeneChip IVT Labeling Kit G GeneChip HWS Kit Protocol	Select Protocol C All C Compatible C Custom C Maintenance G GeneChip IVT Labeling Kit G GeneChip HWS Kit Protocol:	Select Protocol		
Rep:	Step:	Step:	Step:		
Station Module Array Name Probe Array Type	Barcode ID User Protocol Date Ta	me Current Stage Time / Cycle	Temp Time Remaining		

Installing and updating protocols

The fluidics protocols are files that list the steps used to process different types of probe arrays. After installing the GCC Fluidics Control software, you must install the fluidics protocols.

Installing protocols

- From the Files menu, select Install Protocols...
 The Fluidics Scripts Installer opens.
- 2. Click Next.

The Select Software screen appears.

3. Select the software you want to install scripts for and click Next.

The Select Source screen appears.

The screen enables you to:

- Install the protocols from a directory on the file system.
- Install the protocols from the thermofisher.com web site. **Note:** You must be a registered user before using this feature.

To install from a directory:

a. Select the option.

b. Enter the path to the directory or click **Browse** and use the Select Directory dialog box to locate the directory with the scripts.

To install from thermofisher.com:

- a. Select the option.
- b. Enter user name and password.
- 4. Click Next.

The Select Package screen appears.

The screen displays a list of the fluidics scripts packages available from the selected source.

5. Select the package you want to install and click Next.

The Select Protocols screen appears. (Figure 204)

Figure 204 Sel	ect Prot	ocols		
Please select the protocol(s) to	be installed on the	e system and press the Next b	outton.	
Protocol Name	New Version	Version of installed Scri	Calaat All	
DNAarray WS5 450	1	Not Installed	Select All	
EukGE-WS1v4 450	1	Not Installed		
☑ EukGE-W/S2v4 450	1	Not Installed	Llear	
☑ EukGE-W/S2v5_450	1	Not Installed		
FS450 0001	1	1		
FS450_0002	1	1		
FS450 0003	1	1		
FS450_0004	1	1		
FS450_0005	1	1		
FS450_0006	1	1		
Genflex_Sv3_450	1	Not Installed		
Genflexv3_450	1	Not Installed		
GenomeWideSNP5v1_450	1	Not Installed		
✓ Mapping100K∨1_450	1	Not Installed		
Mapping10Kv1_450	1	Not Installed		
C				
		< <u>B</u> ack	<u>N</u> ext >	Cancel

The screen displays a list of the protocols in the selected package with the following information:

- Protocol Name: With check box to select protocol for installation.
- New Version: Version of protocol in selected installation package.
- Version of installed Script: Version of protocol installed on your computer.
- Select the check boxes for the protocols you want to install and click Next. The Summary Screen appears. (Figure 205)



The Summary screen displays information about:

- Selected fluidics scripts
- Source Path
- GCC Target Directory
- GCC Log Path: Location of the log file for this installation.
- 7. Review the information and click Next.

A progress bar displays the progress of the install. (Figure 206)

Figure 206 Progress screen
The Setup W/zard is installing Alfymetrix Fluidics Scripts.
Installing FS450_0005 fluidics files.

When the install is completed, the Finish screen appears. (Figure 207)



8. Click Close.

Editing protocols

You can edit some hybridization and wash (Hybwash) protocols.

Note: Modifications to a Hybwash protocol must be completed before it is run. Protocol changes made during a run do not affect the run in progress.

1. From the Edit menu, select Edit Protocol; or

Click the **Edit** button 🥖.

The Fluidics Protocol Editor dialog box appears. (Figure 208)

Figure 208 Fluidics Protocol Editor				
Protocol Name: FlexFS450_0002	•			
Wash A1 Recovery Mixes	0			
Wash A1 Temperature (C)	30			
Number of Wash A1 Cycles	10			
Mixes per Wash A1 Cycle	2			
Wash B Recovery Mixes	0			
Wash B Temperature (C)	50			
Number of Wash B Cycles	6			
Mixes per Wash B Cycle	15			
Stain Temperature (C)	35			
First Stain Time (seconds)	300			
Wash A2 Recovery Mixes	0			
Wash A2 Temperature (C)	30			
Number of Wash A2 Cycles	10			
Mixes per Wash A2 Cycle	4			
Second Stain Time (seconds)	300 🗸			
Save Defaults Delete	Close			

 Choose the fluidics protocol you want to edit from the Protocol Name drop-down list. The listed protocols are the same ones displayed when you select Custom in the Master and Station controls.

Note: Only the protocols in this list may be edited. All others are defined for specific applications and cannot be customized.

3. Highlight the parameter value you want to change and enter the new value (Parameters values must be within the ranges shown in Table 2 on page 177). Enter a Hybridization Time of zero if only a wash is desired. To omit Wash A or B, enter zero for the Number of Wash A or Wash B cycles.

The FS450 instrument specifications

Fluidics Station Dimensions

(height, depth, width) 40.2 x 41.0 x 71.1 cm or 15 13/16 x 16 1/8 x 28 inches

Product Weight

Approximately 80 pounds or 36.3 kg

Power Input

100 to 240 V~, 3 A 300 watts or less

Main supply voltage fluctuations not to exceed 10% of the nominal supply voltage.

Temperature

Operating: 15° to 30° C Storage (non-operating):-10° to 60° C

Humidity

Operating: 10-90% RH, non-condensing Storage (non-operating):10% to 95% RH

Other

Pollution degree, 2 Installation category, II

Electrical Supply

The electrical supply shall meet the input specified on the instrument label. Voltage fluctuations shall not exceed 10% nominal supply voltage.

Altitude

<2000m

Table 2	Valid ranges	for	hybridization	or	stain	protocol	parameters
	rana rangee			•.		p. 01000.	parametere

Parameter	Valid Range
Hybridization or stain time	0 - 86,399 seconds
Temperature	15 - 50° C
Number of Wash cycles	0 - 99
Mixes per Wash cycle	1 - 99

4. Save the edited protocol:

• To save the parameters under the same protocol name (overwrites the old protocol), click **Save**.

• To save the parameters under a new protocol name, enter a new name in the Protocol Name field, then click **Save**.

This adds the new protocol name to the drop-down list.

5. Click **Defaults** to return the parameter settings to the default values.

6



Scanning cartridge arrays

After processing in the Fluidics Station, the arrays need to be scanned. (Figure 209)



Scanning can be done with the following scanners:

- The GeneChip Scanner 3000 (GCS3000) can be loaded with one chip at a time for scanning.
- The **GCS3000 with AutoLoader (Autoloader)** has a carousel that can be loaded with up to 48 chips. The chips can then be scanned in sequence without operator attention.

The scanners are controlled by with the GCC Scan Control software.

This chapter contains the following sections:

- "GCC scan control software" on page 180
- "Applying Tough-Spots to prevent leaks" on page 185
- "Using GeneChip Scanner 3000" on page 186

IMPORTANT! Read all the material in this chapter before running the scanner.

You can set things up to provide email notification when scans are complete or problems develop. See Appendix E, "Notification e-mails" on page 367 for more information.

GCC scan control software

The GCC Scan Control software is introduced in the following sections:

- "Starting the GCC scan control software"
- "Status window information" on page 182
- "The Status window (Figure 211) displays the following information:" on page 182
- "Setting Up the Scanner ID" on page 184

IMPORTANT! Please make sure that the data roots used in GCC software on the instrument control workstations do not contain files that have non-Thermo Fisher Scientific file extensions (example: DLL, TMP, CPP, ASPX, OUT, etc).

 Starting the GCC
 1. Click the GCC Scan Control icon ☐ in the Launcher; or

 scan control
 Click the Start → Thermo Fisher Scientific → Command Console GCC Scan

 software
 Control.

 The GCC Scan Control window opens (Figure 210).


Components of the GCC Scan Control window:

- Menu bar: Access to functions of the software.
- Tool bar: Quick access to commonly used functions.
- Status Window: Displays list of scanned arrays with information on their status.
- **Status bar**: Displays information about the status of the AutoLoader and the scan in progress.

Hiding or displaying the tool bar

1. From the View menu, select **Toolbar** \rightarrow **Standard Toolbar**.

Adding text labels to the tool bar buttons

1. From the View menu, select **Toolbar** \rightarrow **Text Labels**.

Hiding or displaying the status bar

1. Click \rightarrow View \rightarrow Status Bar. The Status window appears. (Figure 211)



Status window information

Figure 211 Status window	
File Edit View Scanner Help	
Start Add Chips Resume Stop Email Info Hep	
Position Array Name Probe Array Type Barcode ID User D	te & Time Scan Status Data File
1 ALZ_01_PL_01_A_1 Test3 13269 railso A. 2 sample 1_PL_02_A_2 Test3 13285 railso A.	g 22 2007 01:49PM Scan complete C:\Command_Console\Data\Dr Watson Lab\Alzheimer\AL2_01_PL_01_A_2.DAT g 22 2007 01:49PM 22:36% complete C:\Command_Console\Data\Dr Watson Lab\Alzheimer\sample 1_PL_02_A_3.DAT
<	
2 Cartridges Loaded	Autoloader Door: Locked

The Status window (Figure 211) displays the following information:

Position	Position occupied by a given cartridge in the AutoLoader carousel. Completed scans are marked with a green check mark \checkmark . Interrupted or failed scans are marked with a red X 🔀.	
Array Name	Array name assigned to the array.	
Probe Array Type	The probe array type for the scan associated with a given cartridge position.	
Barcode ID	The unique identifier in the barcode for the scan associated with a given cartridge position.	
User	Name of the user (array owner) for the scan associated with a given cartridge position.	
Date & Time	Date and time of the scan.	
Scan Status	 Is The status of the scan. (Autofocus, scanning). This field displays all scanner status strings associated with the scan and retrieved from the scanner. The message strings that may appear in this field are listed below. Note: Not all of the following messages will appear during each AutoLoader run. Autofocus Scan Status - % of lines scanned Scan Complete status Autofocus Errors The array XXX has already been scanned Chip load failures Invalid barcode errors Array does not exist errors Autol order door open errors 	
Data File	Location and name of data file.	

The Default folder is designated by the user as the automatic location of all files created during drop and scan operation, and for DAT and CEL files when the Sample

(ARR) file is located on network data storage.

For more information on Network Data Storage option, see Appendix A, "Networking" on page 338.

For more information about designating the Default folder, see "Specifying a default folder" on page 90.

For more information about transferring data to network data storage, see "Uploading data to network data storage" on page 91.

1. From the Scanner menu, select Information of click the Info button.

The Scanner Information box opens (Figure 212).

Scanner Type:	M10
Scanner ID:	Main Lab Scanner
Serial Number:	M105IM
Hardware Version:	3000
Software Version:	4.0
Filters:	570,532,565,605,655,705
Pixel Sizes:	0.51,0.70,1.09,1.56,2.50
Scans Completed:	
HG-U133A	3

The box displays information on:

- Scanner Type
- Scanner ID, if assigned (see "Setting Up the Scanner ID" on page 184)
- Serial Number
- Hardware Version
- Software Version
- Filters
- Pixel Sizes
- Scans Completed

Reviewing scanner information

7

Setting Up the Scanner ID

You can add an ID label to the scanner which enables you to identify it when email notification is activated.

Adding a label to a scanner

1. From the Edit menu, select Scanner ID...

The Instrument Configuration dialog box opens. (Figure 213)

Figure 213 Instrument Configuration dialog box Instrument Configuration
- Fluidics
Eluidics Stations Installed:
Station Number: 1
Station ID:
Module 1 ID: Module 2 ID:
Module 3 ID: Module 4 ID:
Scanner
Scanner ID:
OK Cancel

- 2. Enter a label for the Scanner in the Scanner ID box.
- 3. Click **OK**.

The label can be seen in the Scanner Information dialog box. (Figure 214)

Figure 214 Scanner Information dialog box		
		_
Scanner Type: Scanner ID: Serial Number: Hardware Version:	M10 Main Lab Scanner	— New scanner ID
Software Version: Filters: Pixel Sizes: Scans Completed:	4.0 570,532,565,605,655,705 0.51,0.70,1.09,1.56,2.50	
HG-U133A	3	
	OK]	



Applying Tough-Spots to prevent leaks

Tough-Spots[™] are chemically inert polyvinyl labels that adhere to all plastics. Applied Biosystems recommends using 3/8-inch circle diameter Tough-Spots to prevent leakage from the array septa.

Before loading the probe array, follow this procedure to prevent the leaking of fluids from the array during scanning.

Even if you have already applied Tough-Spots to the array prior to hybridization or after washing, you must remove the old Tough-Spots and apply new ones before you load them into the AutoLoader.

Thermo Fisher Scientific recommends the use of Tough-Spots P/N 64-0158 or from

USA Scientific, Inc. P.O. Box 3565 Ocala, FL 34478 (800)LAB-TIPS P/N 9185-0000

WARNING! To reduce the risk of leakage, do not use excessively large pipette tips to pierce the septa.

Using Tough-Spots

1. On the back of the probe array, clean excess fluid from around septa (Figure 215).



2. Carefully apply one Tough-Spot over each of the two septa. Press to ensure that the spots remain flat. If a Tough-Spot does not apply smoothly; that is, if you observe bumps, bubbles, tears or curled edges, do not attempt to smooth them out. Remove the spot and apply a new one. (Figure 216)





Using GeneChip Scanner 3000

The GeneChip Scanner 3000 (GCS3000) is used to scan GeneChip probe arrays. It enables you to load and scan one array at a time.



WARNING! ONLY authorized personnel may service this equipment. The GCS3000 Scanner contains an incorporated Class 3B laser. Use of controls or adjustments or performance of procedures other than those specified herein may result in hazardous radiation exposure.



WARNING! The GCS3000 Scanner contains an incorporated Class 3B laser with the following specifications: Wavelength = 532nm +/- 1 nm; Beam Divergence (full angle) = <8mrad; Output Duration = Continuous Wave; Maximum Power Output = 500mW.

Do not remove the cover of the scanner. Use the scanner only as instructed in this User Guide. Do not attempt to service the instrument.

WARNING! A Laser in use during scanning.

IMPORTANT! Read all material in this section before running the GCS3000.

This section contains the following material:

- "Introduction to the GCS3000", below
- "Scanning a probe array with GeneChip Scanner 3000" on page 190
- "Scan Options" on page 194
- "Troubleshooting" on page 195

Laser safety

The laser is equipped with an automatic shutter that inhibits its output beam and ensures safe operation under conditions encountered in normal operation. The instrument covers, the array access port, and protective shutters ensure that during instrument operation no directed or stray laser light leaves the instrument.

IMPORTANT! The scanner is a Class 1 laser product when the laser is enclosed in scanner case. The laser itself is a Class 3B laser product.



DANGER

Laser radiation when open. Avoid direct exposure to laser beam.



CAUTION

Use laser safety glasses when servicing DO NOT STARE INTO LASER BEAM.





Class 1 Laser Product



The green laser is a 532nm solid-state laser. This is a Class 3B laser and has visible outputs greater than 5mw but not more than 500mw. It must never be operated in an exposed manner. Any object in the direct path of the laser beam may be damaged. Eyes and skin can be seriously damaged by direct exposure to, specular reflections from, or diffuse reflections from this laser. If improperly used, a laser of this type can cause fires. When used according to the instructions in this manual and when all covers are in place, the GeneChip Scanner is classified as a Class 1 Laser Product per IEC 60825-1:2007.

Complies with 21 CFR 1040.10 and 1040.11 except for deviations pursuant to Laser Notice No. 50, dated June 24, 2007.

Always take note of laser safety labels; they indicate areas where exposure to laser beams may be hazardous.

Electrical safety The scanner will automatically handle any input voltage from 100 to 240 VAC nominal, 50 to 60 Hz.

Note: The scanner's power supply will auto-detect the input voltage source and configure itself.



The power supply cord is used as the main disconnect device. Ensure that the socket outlet is located and installed near the equipment and is easily accessible.

CAUTION! If you use the scanner in a manner not specified in this user guide, you may impair the protection provided by the equipment.

CAUTION! Do not confuse your company's network connections with the dedicated Ethernet port of the scanner-workstation. The proper scanner connection is located near the top of the workstation.

CAUTION! This 10/100 Base T Ethernet communications port is dedicated to the scannerworkstation interface. You cannot connect the scanner to your company's Ethernet communications network.

IMPORTANT! The reset button is the scanner's circuit breaker. The breaker switch will be tripped whenever the scanner experiences an electrical fault condition. Press to reset. If you cannot reset this switch, contact technical support.



Introduction to the GCS3000

This section contains:

- "Theory of Operation", below
- "Starting the scanner" on page 190
- "Shutting down the scanner" on page 190

Theory of Operation

The GeneChip Scanner 3000 is a wide-field, epifluorescent, near-confocal microscope. The scanner uses a 532 nm solid-state laser to excite probe array fluorophores. This in turn produces an emission wavelength appropriate for the probe array being scanned, which is automatically specified in the scan parameters for the selected probe array. As the surface of the probe array is scanned, a photomultiplier tube collects and converts the fluorescent emissions into an electrical signal. An analog-digital converter in the scanner converts this signal into corresponding numeric values representative of fluorescent intensities. These digital intensity values are collected from discrete areas on the array surface and are stored on the computer workstation as pixels that comprise the image data file (the DAT file). The patented Flying Objective[™] technology represents a radical departure from conventional laser scanners. The optical system comprises a scan arm that rapidly oscillates from side to side scanning the entire width of the probe array in a continuous arc while the probe array is advanced in front of the objective. The acquired image of the array is returned to the computer software as a set of arcs. The software then geometrically corrects these arcs to form a linear image of the array (Figure 218).





The laser source excites the hybridized fluorophores and the photomultiplier system simultaneously captures the resulting fluorescent intensities. The optical components direct the fluorescent beam back through the objective lens, through a dichroic mirror and to the PMT. An analog-digital converter transforms the PMT output into 65536 levels of intensity. Each level of intensity is stored in the software as a 16 bit number (2¹⁶=65536).

The scanner is equipped with an IEC 320 compliant power entry module located at the rear of scanner.

The scanner is equipped with an RJ-45 interface connector compatible with 10/100 Base T Ethernet for communications with the host workstation.

The GCC application controls the scanner. After the scanner has completed a scan, GCC displays a picture of the image in the image window. The software displays the fluorescent intensity values from each pixel within the probe array feature in a grayscale or pseudo color mode and superimposes a grid on the image to delineate the probe cells.

GCC analyzes the image and derives a single intensity value for each probe cell on an array. This data is automatically generated and saved to the cell intensity file.

Starting the scanner

1. Press the on/off (I/O) switch on the front panel.

The scanner's onboard computer boots up. The bootup process takes a few minutes. During this time both the yellow and green light will be on. The scanner enters the laser warm-up state. During this warm-up time, the green light will turn off and the yellow light will remain on. You must wait 10 minutes for the laser to stabilize.

Shutting down the scanner

1. Close the GCC software. This is the best way to shut off the laser. Alternately, press the I/O (on/off) button on the front panel to turn off the instrument.

Note: The laser also has a sleep mode that activates after 1 hour of inactivity.

Scanning a probe array with GeneChip Scanner 3000 This section shows you how to scan a GeneChip probe array using the GeneChip Scanner 3000.

Scanning the probe array

- 1. Turn on the Scanner-AutoLoader (see "Starting the scanner", above).
- 2. Start the GCC Scan Control Software (see "GCC scan control software" on page 180).
- Click the Start button ➡ in the main tool bar; or Select Scanner Start Scanner from the menu bar. The Scanner dialog box opens. (Figure 219)



Figure 219 Scanner Dialog box
Barcode: Sample Attribute File Name: Array Name:
Probe Array Type: Pixel Size: Data Location: Start Laser is On Load/Eject Cancel

At this point, you can choose from these options:

• If your array has a valid barcode, you can scan the barcode on the probe array into the barcode field. The software will retrieve the sample file and array name associated with the barcode.

If the barcode is not associated with an existing Sample file and array, a sample file will be created during scan using Drop and Scan.

- If your array does not have a valid barcode, you can manually select an array as described below:
- a. Select the Sample file name for the probe array you want to scan from the **Sample File Name** drop-down list.
- b. Select the array name of the probe array to be scanned from the **Array Name** drop-down list.

The **Probe Array Type** field automatically displays the probe array type that was entered while creating the Sample file.

4. Click Start in the Scanner dialog box.

The Start window appears. (Figure 220)

Figure 220 The Start Scanner dialog box Image: Start Scanner dialog		
GeneChip Scanner		
Load your samples in the autoloader, then click OK or press Enter		
Array at room temperature		
Allow rescans		
OK Cancel		

If you want to skip the warm-up period before scanning the first probe array, keep the default check-mark in the **Array at room temperature** check box. If you want to allow rescans, click the **Allow rescan** check box.



5. Click **OK** to start the run.

The GeneChip Scanner dialog box appears. (Figure 221)

Figure 221	Scanner dialog	box
Load you	r sample, then click OK o	r press Enter
OK.) Options	Cancel

The scanner door opens and the chip transport mechanism raises to accept a probe array.

6. Load the probe array (Figure 222) into the scanner chip transport mechanism. Insert the probe array into the chip transport mechanism such that the front of the probe array (label side) faces to the rear of the scanner.

Note: The scanner will enter Park mode if it is unattended for 15 minutes and will enter standby, or sleep, mode if it is unattended for 60 minutes (45 minutes after entering Park mode). The green light will turn off and the yellow light will turn on. To reactivate the laser, click **Turn Laser On** in the scanner dialog box and wait 10 minutes.



CAUTION! Do not force the probe array. If the array does not drop easily into the chip transport mechanism, eject the array and try again. If this does not remedy the situation, see"Troubleshooting" on page 195 or call technical support. Also, if a probe array becomes lodged in the scanner, you can manually remove it. For more information, see "Manually removing a lodged/stuck probe array" on page 196.

In addition, you cannot modify the scanner settings. GCC automatically selects the appropriate settings based on the probe array type specified during experiment setup.



Figure 223 Loading the probe array into the chip transport mechanism. Note that the front of the probe array faces to the rear of the scanner.



 Click **OK** in the GeneChip Scanner dialog box to start scanning the probe array. During the scan, the green light will flash, and the yellow light will be off.

After the scan starts, the software will start with the auto-focus routine. Data collection starts after successful completion of auto-focus. During the pre-scan state, when auto-focus is complete, but before data collection has started, the software will count downwards.

Note: When multiple emission filters are used during the scan process, the software will display the scan with a letter followed by the percentage of scan completed. The letter identifies the scan associated with the emission filter.

After the scan is completed, GCC:

- Saves the image data.
- Aligns a grid on the image to identify the probe cells.
- Computes the probe cell intensity data.
- Ejects the probe array.



Note: If you leave the scanner idle for an additional 15 minutes, the scanner will also enter "Park" mode. The yellow light is off and the green is light on. The chip transport mechanism will retract and the scanner door will close. You must click the **Eject Chip** button to open the scanner door and raise the chip transport mechanism.

Note: You can track the progress of the grid alignment and cell intensity computation in the GCC Viewer. For more information see Chapter 9, "Using the GCC viewer" on page 267.

Scan Options This section describes various options when using the GCS3000:

- "Scanning Four-Color Arrays"
- "Stopping a Scan" on page 194

Scanning Four-Color Arrays

The four color scans are performed on GeneChip arrays that have been configured for use with four emission filters. The four emission filters are specified in the GCC scan parameters. when performing a multi-filter scan, GCC scans the array with different emission filters, using the order specified for the array.

A DAT file is created for each of the emission filter scans. To distinguish the different scans, GCC appends a suffix of A, B, C, or D to the DAT files. Different file naming conventions are used in the case of a rescan of an array, depending upon whether the array was manually loaded.

When running multiple scans on an array, the scanner performs autofocus only once, prior to the first scan. This is true whether the scans are performed as part of a fourcolor scan or as a re-scan.

Aborting a scan with a manually loaded array

If scanning is aborted on a manually loaded array, the emission filter scan in progress continues until it is complete, and the DAT data for the completed scans are saved. When the scan is resumed, GCC auto-focuses the scanner and then re-scans and recreates a DAT file for each emission filter scan, overwriting the previously created DAT files.

Stopping a Scan

- 1. Click the **STOP** button *O* or select **Run Stop Scanner** from the menu bar.
- 2. At the prompt, click **Yes** to stop the scanner or **No** to cancel stopping (Figure 224).

The Stop command will abort the run in progress and result in uneven photo-bleaching to the array being scanned.
Are you sure you want to stop the scanner?



CAUTION! If you click Yes, the data from a partial scan will be lost. This is different from using earlier software or scanner versions where you could save the data from a partial scan.

If you rescan a probe array that has been partially scanned, the previously scanned area of the probe array may experience fluorophore bleaching. This will result in non-uniform fluorescence intensity across the probe array.

3. After you stop a scan, the scanner will automatically eject the array.

Note: The scanner dialog box has an eject array button. This is reserved for ejecting an array after the scanner goes into sleep mode or when you must manually eject the array for any other reason. If the probe array becomes stuck, see "Troubleshooting" or call technical support.

Troubleshooting

Table 3 Troubleshooting tips

Problem	Possible Cause	Corrective Action
No image when scanning	Power off or cable loose	Check all connections and power.
	Loss of laser power	Contact technical support.
Intermittent problems scanning	Loose cable	Check all rear connections.
Scanner fails with probe array inside	Power failure	Manually extract probe array. Check all connections to scanner. Turn scanner on, restart software.

For additional troubleshooting information, see:

- "Issues relating to the scanner's operation" on page 195
- "Manually removing a lodged probe array" on page 218

Issues relating to the scanner's operation

The table below lists some issues and problems that you may encounter while using



the GCS3000.

Issue	Explanation
If communications are interrupted during a scan (by a faulty cable connection or power being lost at the scanner, for example)	GCC will properly note the failure and present a message "Cannot connect to Scanner." However, there are two issues to note. First, GCC will report such a failure only after a network time-out of about 30 seconds. Second, rarely, if communications have been lost, GCC and the Scanner may not be able to automatically restore communications once the problem is rectified, and both may become unresponsive. To restore proper operation, verify that the scanner is on, that communication cables are
	properly connected, and close and restart Microsoft [®] Windows [®] then restart GCC. If the system remains unresponsive, disconnect and reconnect power to the scanner, restart the scanner normally, close and restart Microsoft [®] Windows [®] and GCC.
Repeated attempts to send commands (Start, Turn Laser On, etc.) from GCC to the Scanner while GCC is reporting the scanner "Offline" may result in GCC becoming unresponsive until communications are restored	If communications cannot be re-established, please follow the recommendations of item 1
If the Scanner experiences multiple auto-focus failures, the system may enter an unresponsive state.	Follow the recommendations of item 1 to restore communications and correct operation.
Laser warm-up lasts for ten minutes, during which time the "Turn Laser On" button will remain unchanged and GCC will display the status message "Warm-up".	Simply note that this is normal operation.
If no array is inserted and a scan started.	The scanner will attempt go through the first parts of the auto-focus routine and then report "Failed to find chrome border".
The scanner should be in the pa	rk mode to eject the array.
Auto focus will fail if salt deposits accumulate on the array.	Use Tough-Spots to prevent leaks in the GeneChip probe array. See the quick reference card, p/n 08-0076.

CAUTION! Heavy object. Two people are required to lift the scanner.

Manually removing a lodged/stuck probe array

In the event that a probe array becomes lodged in the array transport mechanism, follow the procedure outlined below.

- 1. Turn off the scanner.
- 2. Insert a paper clip or small Allen wrench into the rescue hole on top of the scanner and press to partially lift the array loading door.





- 3. Using your fingers, gently lift the front edge of the door. As you lift the front edge, lift the back edge approximately 1/4" to open the door straight up to expose the rescue screw in the front.
- 4. Using a standard (-) screwdriver, turn the rescue screw clockwise to raise the array transport mechanism.
- 5. Continue to turn the screw until the probe array ascends sufficiently to grab it.



Note that the screw is fine pitched and requires a number of turns. Stop if you encounter screw resistance. Do not over torque.

6. When the array has ascended sufficiently, remove it.





- 7. Re-screw the array transport mechanism until it descends completely, or until you encounter resistance. Do not over torque.
- 8. Close the door.



GCS3000 Specification

Item	Parameter	Value
Weight	Shipping	approx 74 pounds (35.4 Kg)
	Free -standing	63 pounds (28.6 Kg)
Dimensions	Width	-13.25 in
	Depth	-27.5 in
	Height	-18.25 in
Power	Voltage Current Line Frequency	100 - 240 V – 4 - 2 A 50 - 60 Hz
Working Environment	Temperature	59°F-85°F (15°C-30°C)
	Humidity	10-90% Non-condensing
	Clearance	2 in.(5 cm) on side, back and top
	Pollution Degree	2
	Installation Category	Ш
	Altitude	<2000m
Electrical Supply	Provide voltage, frequency or power rating per unit label	
Main Supply Voltage Fluctuations	Are not to exceed ±10% of the nominal supply voltage	

GCS3000 Specification table:



Using the GCS3000 with AutoLoader

The GeneChip Scanner 3000 with AutoLoader (AutoLoader) is similar to the GCS3000 with the addition of a carousel autoloader, designed expressly for scanning multiple GeneChip probe arrays. The AutoLoader can scan up to 48 probe arrays automatically without operator presence.



Laser in use during scanning.



Introduction

For more information about the scanner, see "Introduction to the GCS3000" on page 189.

Starting the AutoLoader

To turn on the AutoLoader:

• Turn on the Scanner-AutoLoader by pressing the on/off (I/O) switch on the front panel.

The scanner's onboard computer boots up. The bootup process takes a few minutes. During this time both the yellow and green light will be on. The scanner enters the laser warm-up state. During this warm-up time, the green light will turn off and the yellow light will remain on. You must wait 10 minutes for the laser to stabilize.

Shutting down the scanner

- 1. Close the GCC software. This is the best way to shut off the laser.
- 2. Press the I/O button on the front panel to turn off the instrument.



This section shows you how to scan a GeneChip probe array using the GeneChip Scanner 3000 with AutoLoader.

Scanning chips using the AutoLoader

1. Turn on the AutoLoader by pressing the on/off (I/O) switch on the front panel.

The scanner's onboard computer boots up. The bootup process takes a few minutes. During this time both the yellow and green light will be on. The scanner enters the laser warm-up state. During this warm-up time, the green light will turn off and the yellow light will remain on. You must wait 10 minutes for the laser to stabilize.

2. Load your cartridges into the carousel (up to 48). Note that only one orientation is possible (Figure 229).

Cartridges should be loaded into the carousel starting at position #1. Additional cartridges need not be contiguous. A run will stop after 48 cartridges OR when the same barcode is read within the same run.

Figure 229 Loading the array into the chip carousel. Each slot is numbered, 1 through 48, and each array can fit in only one orientation



 Load the carousel into the AutoLoader by inserting the carousel into the AutoLoader and turning the carousel until the alignment pin seats into the alignment hole. (Figure 230)



- 4. Turn the carousel clockwise until the carousel mounting key flat seats gently into the AutoLoader alignment key. You may have to turn the carousel several times before it will seat into the alignment pin and alignment key. When seated properly, the carousel will be flush with the AutoLoader housing.
- 5. Close the AutoLoader door. (Figure 231)



Note: The seating of the key flat is confirmed by a gentle falling of the carousel into the key.

Note: If all probe arrays have valid, associated barcodes, you can run the AutoLoader in auto-mode.

Note: If there exists an identical barcode within the database from an earlier AutoLoader run, and you want to rescan the current probe array with that same barcode, check the Allow Rescans box. This will create additional DAT files. The original DAT file WILL NOT BE OVERWRITTEN. A new DAT file is created, and the file name for the new file has an underscore and incremental number added to it, beginning with _2. If the AutoLoader encounters the same barcode within the same run, the run will terminate.

- Start the GCC Scan Control software (see "Starting the GCC scan control software" on page 180).
- 7. Set the default settings.
 - a. Click Edit Options.
 - b. Clear the Enable Manual Mode check box.
 - c. Click OK.



Figure 232 Scanner Options dialog box with Enable Manual Mode check box cleared
☑ Turn on <u>L</u> aser at startup
Enable Manual Mode
🔲 Disable Autoloader
OK Cancel

 Click the Start button finite main tool bar; or Select Scanner Start Scanner from the menu bar.

The Start window appears. (Figure 233)

Figure 233 The Start Scanner dialog box in automode					
Load your samples in the autoloader, then click OK or press Enter					
Arrays in carousel positions 1-4 at room temperature					
Allow rescans					
OK Cancel					

If you want to skip the warm-up period before scanning the first probe array, keep the default check in the **First four arrays at room temperature** box.

- 9. Click **OK** in the Start Scanner dialog box to start the run.
 - The AutoLoader blue indicator light will light up signifying that the AutoLoader door is now locked.
 - The carousel automatically homes itself and performs inventory to determine the number and position of cartridges present.
 - The scanning run begins. During the scan, the green light will flash, and the yellow light will be off.
 - The AutoLoader completes the autofocus operation before scanning each of the probe arrays. This takes approximately two to three minutes. The scanner cannot be stopped during this period.
 - The run will stop automatically when the last array is scanned.
 - At the completion of each scan, the GCC software will attempt grid alignment. If it is successful, the scan data will be automatically advanced to the Grid Alignment processing state. The progress of the scan data can be tracked using the Review Window of the GCC Viewer (see Chapter 9, "Using the GCC viewer" on page 267).
 - The progress of each scan is displayed in the Scan Status window (Figure 234).



E.											
	Figu	ire 234 Sc	an S	tatus	winde	ow durir	ng aut	toloader run.			
	•						0				
	File Edit	View Scanner Help									
			0			?					
	Start	Add Chips Resume	Stop	Email	Info	Help					
	Position	Array Name		Probe Ar	rray Type	Barcode ID	User	Date & Time	Scan Status	Data File	
	2 1 2	ALZ_01_PL_01_A_1 sample 1_PL_02_A_2		Test3 Test3		13289 13285	rallso rallso	Aug 22 2007 01:49PM Aug 22 2007 01:49PM	Scan complete 22.36% complete	C:\Command_Console\Deta\Dr Watson Lab\Alzheimer\Alz_01_PL_01_A_2.DAT C:\Command_Console\Deta\Dr Watson Lab\Alzheimer\sample 1_PL_02_A_3.DAT	
	< 2 Cartrido	es Loaded						Aub	inader Door: Locked		>
								, inde			

 The window displays a list of the arrays as they are being scanned with the information displayed in the Status window (see "Status window information" on page 182)

After the scan is completed, GCC:

- a. Saves the image data to an image file (*DAT).
- b. Ejects the probe array.
- c. Aligns a grid on the image to identify the probe cells.
- d. Automatically computes probe cell intensities and saves the data to the cell intensity file (*CEL).

Note: You can track the progress of the grid alignment and cell intensity computation in the GCC Viewer.

Arrays with barcodes that are not associated with a Sample file and array will have a sample file created using Drop and Scan.

The AutoLoader will **skip** probe arrays if the AutoLoader encounters:

- Arrays with unreadable or invalid barcodes or without barcodes.
- Arrays that have been previously scanned if the Allow Rescans check box is cleared.
- 10. Close the GCC Scan Control software. This is the best way to shut off the laser.
- 11. Press the I/O button on the front panel to turn off the instrument.



Special scan options

The following sections describe various options for running the scan:

- "Drop and scan" on page 206
- "Stopping an AutoLoader run" on page 206
- "Adding cartridges during a run" on page 207
- "Scanning a Probe Array in Manual Mode" on page 210
- "Ejecting a probe array" on page 212
- "Using GCC with the AutoLoader disabled" on page 212
- "Scanning four-color arrays" on page 213
- "Terminating a scan run" on page 214

Drop and scan

The Drop and Scan feature lets you scan a set of GeneChip probe arrays without first creating a Sample (ARR) file for them. A Sample file is created automatically during Drop and Scan, with the probe array barcode used as the file name.

- 1. Start the GCC Scan Control software.
- 2. Start the scanner.
- 3. Load the arrays in the scanner.
- 4. Click the Start button.

If the arrays have valid barcodes, they are scanned. The ARR, DAT, and CEL files are named using the barcode and placed in the designated Default folder.

For more information about the Default folder, see:

- "Default folders" on page 33
- "Specifying a default folder" on page 90

If the scanner cannot read the barcode, or if there are no library files on the system for chips with that part number, the chip is ejected and an error notice appears.

Stopping an AutoLoader run

The Stop button is only available after you have clicked the Start button. Click this button if you want to abort a scan or run in progress.

Note: If you stop the scanner while a probe array is in the process, you will lose all scan information from that probe array. If you rescan the array, it may be affected due to uneven photo-bleaching. This could potentially make the data from the array difficult to compare to other array data.

- Click the STOP tool bar button Or select Scanner Stop Scanner from the menu bar.
- 2. At the prompt, click **Yes** to stop the scanner or **No** to elect not to stop the AutoLoader run.



Figure 235	Stop AutoLoader prompt
The Stop in unever Are you s	command will abort the run in progress and result photo-bleaching to the array being scanned. ure you want to stop the scanner? Yes No

A window displays the message "The scanner will not stop until autofocus has finished."

3. Click OK.

After you stop a scan, the scanner automatically ejects the array.

Adding cartridges during a run

The software provides you with a button that will enable you to unlock the AutoLoader door and add additional probe array cartridges while in the middle of an AutoLoader run. You have two choices:

- To add cartridges immediately even while a scan is in progress (in which case the DAT file is discarded and replaced with a newly collected one after the AutoLoader run is resumed).
- To add cartridges after a scan has completed (in which case the DAT file is saved).

Note: The Add Chips button is enabled only after the AutoLoader has started a run in automatic mode.

Interrupting a scan in progress

Note: If you stop the scanner while a probe array is in the process, you will lose all scan information from that probe array. If you rescan the array, it may be affected due to uneven photo-bleaching. This could potentially make the data from the array difficult to compare to other array data.

1. Click the **Add Chips** button **()**, or select **Run Add Chips** from the menu bar. The Add Chips Options dialog box opens. (Figure 236)

Figure 236 The Add Chips box	s Options dialog
Warning: Adding chips without completi	ing the scan will
cause the chip currently being scanned	to be rescanned.
Add Now Add after Scan	Cancel

2. Click Add Now.

The blue AutoLoader indicator light will turn off signifying that the AutoLoader door is now unlocked.



If a scan is in progress, the software will continue to record the scan. However, to avoid the possibility of generating a corrupt DAT file, it will discard that scan that was in progress when the door was opened.

- 3. Open the door and add probe array cartridges to the carousel.
- 4. Close the scanner door.

The following window appears. (Figure 237)

Figure 23	7 Resume notice
Press	the Resume button to continue the autoloader run

- 5. Click **OK.**
- Click the Resume button; or select Run Resume. The Notice dialog box opens. (Figure 238)

Figure 238	Notice dialog box
Load your sample or press Enter	s in the autoloader, then click OK
🔽 Arrays in caro	usel positions 1-4 at room temperature
Allow rescans	
0	K Cancel

7. Select the Allow Rescans option, if desired, then click OK.

The blue AutoLoader indicator light turns on signifying that the door is locked. The software homes the carousel and inventories the number of present probe arrays. The carousel then moves to that last previously scanned probe array (when the door was opened) and continues the scanning run by rescanning that probe array.

The array is rescanned and a new DAT file overwrites the previous DAT file.

IMPORTANT! Do not load an array into the same carousel position that was occupied by the array that had just been scanned, i.e., do not replace cartridges.

Adding chips without interrupting a scan

 Click the Add Chips button , or select Run Add Chips from the menu bar. The Add Chips Options dialog box opens. (Figure 239)



Figure 239 buttons	The Add Chips s	selection
Warning: Ad cause the ch Add Now	ding chips without completing ip currently being scanned to	the scan will be rescanned. Cancel

2. Click Add after scan.

The Interrupt After Scan Complete notice appears. (Figure 240)

Figu	re 240	Complete Scan notice
⚠	The autol	pader run will stop after the scan is complete.

3. Click **OK**.

The AutoLoader will wait until the current probe array has undergone the autofocus and scan procedures before unlocking the door.

The blue AutoLoader indicator light turns off when the AutoLoader door is unlocked.

- 4. Open the door and add probe array cartridges.
- 5. Close the scanner door.

The Resume Notice dialog box opens. (Figure 241)

Figure 24	1 Resume notice
Pre	s the Resume button to continue the autoloader run

The GCC status bar displays a "waiting to start" status.

- 6. Click OK.
- 7. Click the Resume 📷 button; or
 - Select $\textbf{Run} \rightarrow \textbf{Resume}.$

The Run Options dialog box opens. (Figure 242)



Figure 242 Run options dialog box
Load your samples in the autoloader, then click OK or press Enter
Arrays in carousel positions 1-4 at room temperature
Allow <u>r</u> escans
OK Cancel

8. Select the Allow Rescans option, if desired, and click OK.

The blue AutoLoader indicator light turns on signifying that the door is locked. The software homes the carousel and takes inventory of the probe array cartridges present. The carousel then proceeds to the next array position following the previously scanned probe array. The AutoLoader continues the run from that array position.

Note: If you click the **Cancel** button in the Run Options dialog box, the AutoLoader will not resume the scan.

Scanning a Probe Array in Manual Mode

In the AutoLoader Automode, each probe array requires a valid barcode in order to be scanned. The manual mode feature enables you to scan one probe array at a time without the requirement of a barcode. This is useful if you must scan probe arrays that have invalid or absent barcodes.

- 1. Set the scanner options.
 - a. From the Edit menu, click **Options**.

The Scanner Options dialog box opens. (Figure 243)

- b. Check Enable Manual Mode.
- c. Click OK.

Figure 243 Scanner Options dialog box, Enable Manual Mode checked		
Turn on Laser at startup Enable Manual Mode Disable Autoloader OK Cancel		

 Click the Start button ; or Select Scanner Start Scanner from the menu bar. The Scanner dialog box opens. (Figure 244)



Figure 244 Scanner Dialog box
Barcode:
Sample Attribute File Name:
Array Name:
Probe Array Type:
Pixel Size: Data Location:
Start Laser is On Load/Eject Cancel

At this point, you can choose from a number of options:

- You can click Start without selecting an array name. If your array has a valid barcode, the software will get the barcode from the array in the AutoLoader and select the correct Sample file and Array name.
- If your array has a valid barcode, you can scan the barcode on the probe array in to the barcode field. The software will retrieve the Sample Attribute File associated with the array.
- If your array does not have a valid barcode, you can manually select an array as described below:
- Select the Sample file name for the probe array you want to scan from the Sample File Name drop-down list.
- Select the array name of the probe array to be scanned from the Array Name drop-down list.

The **Probe Array Type** field automatically displays the probe array type that was entered during experiment setup.

3. Click Start in the Scanner dialog box.

The Start dialog box appears. (Figure 245)

Figure 245	The Start Scanner dialo	og box
Load your sa press Enter	amples in the autoloader, then click	OK or
🗖 Array at ro	oom temperature	
Allow reso	cans	
	OK Cancel	



Note: If you want to skip the warm-up period before scanning the first probe array, keep the **Arrays at room temperature** check box marked as checked.

Note: You can eject or load an array by clicking on the Load/Eject button at any time except when the scanner is engaged in the autofocus operation or the scanning run.

4. Load the probe array into slot number 1.

Note: The array slot at position number 1 is the only slot available in Manual Mode.

 Click OK in the Start Scanner box (Figure 245) to start the autofocus routine. This takes approximately two to three minutes. The scanner cannot be stopped during this period.

During the scan, the green light will flash, and the yellow light will be off.

After the scan is completed, GCC:

- a. Saves the image data to an image file (DAT).
- b. Aligns a grid on the image to identify the probe cells.
- c. Automatically computes probe cell intensities and saves the data to the cell intensity (CEL) file.

Note: You can view the status of the cell intensity computation in the GCC Viewer.

d. Ejects the probe array.

Ejecting a probe array

The probe array will automatically eject after a run.

Using GCC with the AutoLoader disabled

If you have a working scanner but the AutoLoader is not operating, you can still use the scanner, but you must check the Disable AutoLoader option in the Defaults window. This will disable the AutoLoader and enable you to use the scanner alone as you would in manual mode.

- 1. From the Edit menu, click **Options**.
- The Scanner Options dialog box opens. (Figure 246)
- 2. Check Disable AutoLoader.
- 3. Click OK.

Figure 246 Disable AutoLoader checked		
 ✓ Turn on Laser at startup ✓ Enable Manual Mode 		
Disable Autoloader OK Cancel		



A window will appear asking that you reboot the scanner.

Figure 247	Reboot notice
Autoloa	der Mode had Changed. Please Reboot Scanner

- Press the scanner front panel I/O button once to turn off the scanner. Wait a few moments, the press the I/O button to turn on the scanner.
- 5. Open the AutoLoader door.
- 6. Manually load a probe array into the slot.
- 7. Close the AutoLoader door.
- 8. Scan the probe array in the same manner as the AutoLoader in manual mode. See "Scanning a Probe Array in Manual Mode" on page 210.

After scanning the probe array, you must manually remove the probe array from the AutoLoader. See Steps 7 though 13 in "Manually removing a lodged probe array" on page 218.

Scanning four-color arrays

Four color scans are performed on GeneChip arrays that have been configured for use with four emission filters. The four emission filters are specified in the GCC scan parameters. when performing a multi-filter scan, GCC scans the array with different emission filters, using the order specified for the array.

A DAT file is created for each of the emission filter scans. To distinguish the different scans, GCC appends a suffix of A, B, C, or D to the DAT files. Different file naming conventions are used in the case of a rescan of an array, depending upon whether the array was manually loaded (see below) or loaded using the autoloader.

When running multiple scans on an array, the scanner performs autofocus only once, prior to the first scan. This is true whether the scans are performed as part of a fourcolor scan or as a re-scan.

Aborting a four-color scan with a manually loaded array

If scanning is aborted on a manually loaded array, the emission filter scan in progress continues until it is complete, and the DAT data for the completed scans are saved. When the scan is resumed, GCC autofocuses the scanner and then re-scans and recreates a DAT file for each emission filter scan, overwriting the previously created DAT files.

Aborting a four-color scan when using the autoloader

If scanning is aborted on an array loaded using the autoloader, the emission filter scan in progress continues until it is complete, and the DAT data for the completed emission scans are saved. When the scan is resumed, GCC auto focuses the scanner and then re-scans and re-creates a DAT file for each emission filter scan. GCC does not overwrite the previously created DAT data, but creates a new set of DAT files, adding a suffix of "_nX" to the DAT file name, where n identifies the rescan number and 'X' is the letter assigned for the emission filter. A 4-color array scanned a second time will produce DAT files with the following suffixes: _2A, _2B, _2C, _2D.



Note: When using the "Add Chips Now" function of the autoloader, if the door is opened in the middle of a scan acquisition, GCC treats the scan as an abort request. After the emission filter scan in progress completes, scanning halts and the DAT and CEL files for the completed emission filter scans are saved. Upon resume, the GCC auto-focuses the scanner and rescans the array for each emission filter. To avoid the rescan of the array, it is recommended that the "Add Chips Later" function be used.

Autorotation: The AutoLoader is equipped with a heater to warm up the cartridges prior to scanning in order to reduce condensation and fogging of the probe array window. This autorotation routine is used for temperature stability but only after the AutoLoader run is complete or during a power failure as described below.

Autorotation

Autorotation occurs during a power failure only if the uninterrupted power supply (UPS) is included as an accessory. The UPS provides power to the scanner/ AutoLoader during a power failure. If the power fails during the scan of an array, that scan is completed and then the system turns off the heater and enters the autorotation mode to conserve power and cool the chips in the carousel. The system will also attempt to send an e-mail to notify the user of the power failure.

During an AutoLoader run, the carousel is rotating as the chips are processed to introduce the next array to the scanner, so autorotation is not needed. After the AutoLoader run is complete the heater is turned off and the carousel is rotated to get even cooling of the chips.

Terminating a scan run

The AutoLoader run will terminate under certain normal circumstances. Table 4 outlines under what conditions a scan run will or will not terminate.

Table 4	Summary	of scan run	termination	conditions
---------	---------	-------------	-------------	------------

The scan run will terminate if:	The scan run will not terminate if:
You press the Stop button. Caution: If you stop the scanner while a probe array is in the process, you will lose all scan information from that probe array. If you rescan the array, it may be affected due to uneven photo- bleaching. This could potentially make the data from the array difficult to compare to other array data.	You check Allow Rescans box. When the AutoLoader encounters a probe array that was previously scanned in an earlier run, it will rescan that probe array and will create additional DAT files (DAT1, DAT2, etc.).
The AutoLoader detects a probe array with the same barcode in the current run, i.e., in the currently loaded carousel. The probe array will not be rescanned.	You clear the Allow Rescans box. When the AutoLoader encounters a probe array that was previously scanned in an earlier run, it will log the probe array but will not rescan it. It will continue the run.



Table 4 Summary of scan run termination conditions

The scan run will terminate if:	The scan run will not terminate if:
The AutoLoader detects 48 scanned cartridges in the same run.	You click the Add Now button. The AutoLoader door will unlock to accept new probe array cartridges. The scan in progress will complete. When you close the door and continue, the AutoLoader will home, take inventory and move to the same probe array that was in the process of being scanned when the door was opened. It will discard the earlier DAT file and rescan that probe array. Note: this has nothing to do with the Allow Rescans check box.
	You click the Add After Scan button. The AutoLoader door will wait until the scan in progress is complete then unlock the door. When you close the door and continue, the AutoLoader will home, take inventory and move to the next probe array from that which was in the process of being scanned when the door was opened.

Troubleshooting

Troubleshooting tips are given in the table below and in the following sections:

- "AutoLoader error messages" on page 216
- "Manually removing a lodged probe array" on page 218

Problem	Possible Cause	Corrective Action
No image when scanning	Power off or cable loose	Check all connections and power.
	Loss of laser power	Contact technical support.
	Image display disabled	Enable image display
Intermittent problems scanning	Loose cable	Check all rear connections.
Scanner fails with probe array inside	Power failure	Manually extract probe array. Check all connections to scanner. Turn scanner on, restart software.
Carousel does not automatically home	 Check for stuck array Carousel not seated on D ring Alignment Pin not engaged in Carousel Door is open or ajar Door is open when blue LED is off. 	
Carousel does not rotate	 Door is open or ajar System is warming up, array in heater Carousel not seated on D ring Alignment Pin not engaged in Carousel Laser in Scanner is warming up. GCC has Start grayed out in this case 	
Carousel misses next array	Array UP sensor not working, call technical support.	
Stuck array		See "Manually removing a lodged probe array" on page 218
AutoLoader freezes up	Door is open or ajar	

Problem	Possible Cause	Corrective Action
AutoLoader overheats	Heater Failure	Call technical support.
	• TE failure	
	• TE hot fans vent blocked	Call technical support.
Autofocus routine fails to conclude		 Try to rescan array. Check for salt on chrome border. If still error, call technical support.
The array does not descend into scanner.	 Carousel not seated correctly Door is open or ajar Heater is waiting until array is at temperature. 	

AutoLoader error messages

The following error messages indicate a serious malfunction of the scanner with AutoLoader. Your probe arrays, or the data generated from them, may be at risk. You should shut down the AutoLoader and remove the carousel. Do not continue to use the AutoLoader in Automode and call technical support. However, if the AutoLoader appears to be operating normally, you can continue to use the AutoLoader in Manual Mode. See "Scanning a Probe Array in Manual Mode" on page 210.

HEATER_LOW	"Warning: The warming chamber temperature is low. Refer to the troubleshooting guide."
COLD_CHAMBER_LOW	"Warning: The cold chamber temperature is low. Refer to the troubleshooting guide."
COOL_HOTSIDE_HIGH	"Warning: The cooler hot-side temperature is high. Refer to the troubleshooting guide." Note: Before calling technical support, check around the ventilation vents to ensure
	that nothing is blocking them.
COLD_CHAMBER_HIGH	"Warning: The cold chamber temperature is high. Refer to the troubleshooting guide."
	Note: Before calling technical support, check the AutoLoader door to ensure that it is not open.
HEATER_HIGH	"Warning: The warming chamber temperature is high. Refer to the troubleshooting guide."

E-mail messages

If the e-mail system is enabled, the instrument control software sends an e-mail alert for conditions that may occur during an AutoLoader run.

Note: For information on enabling the email system see Appendix E, "Notification emails" on page 367

In case of a fatal error:

- 1. The software sends an e-mail to the specified set of e-mail addresses or to the Outlook distribution list.
- 2. The software provides you with the ability to send an e-mail without your intervention.

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- 3. Each e-mail message contains the following information:
 - a. Date and Time
 - b. Scanner ID
 - c. All experiment information displayed in the status window. You select error messages to be sent in the e-mail configuration.



Manually removing a lodged probe array

In the event that a probe array becomes lodged in the array transport mechanism, follow the procedure outlined below.

- 1. Turn the AutoLoader off and remove the power cord from the back of the unit.
- 2. Open the AutoLoader door on top of the unit.
- 3. Remove the carousel from the system. (Keep cartridges in carousel at proper temperature while recovering the array still in the scanner).
- 4. Remove the hole plug, which is just in front of the array slot in the base piece of insulation. In Figure 248, the screwdriver is inserted into this hole.



- 5. Using a standard, flat (-) screwdriver, (13-0257) gently slide it down through the hole making sure not to damage the shaft and spring that are protruding into the hole. When the screwdriver stops, it should be in contact with the scanner Y stage screw. Slowly turn the screwdriver until you feel it engaging the slot on the screw of the scanner Y stage.
- 6. Slowly turn the screw clockwise until it hits a hard stop and cannot turn further. (Do not try to turn it further or use excessive force because it will break the Y stage in the scanner). The Y stage has now ascended to its maximum position.
- 7. Using your fingers, slowly slide the slot pin, which is sticking through the slot in the base piece of insulation, to the right until it stops. You should see the little pinch rollers near the array slot close a little as you do this. (Figure 249)





 Insert a 3/16" hex driver (13-0255) into the hole that is located on the front of the AutoLoader housing on the left. You should feel it engage a coupling. (Figure 250)



- 9. Turn the hex driver counter clock wise until you see the array appear through its opening. (The array should stay up if you stop turning the hex driver). If you don't see the array after turning the hex driver ten seconds go to step 11.
- 10. Grab and hold the array with your fingers. Using your other hand slowly slide the slot pin (Step 7) back to the left. This should open up the pinch rollers. Pull the array out.

If you do not see the array after turning the hex driver for 10 seconds, stop.



11. Using tool (13-0256) (Figure 251) with the hook down and toward the back, slide it vertically down against the front of the array opening, about 1.5 inches. (There is a small groove made for this tool in the middle of the front array guide).



12. Pull the top finger grip of the tool toward the front of the unit, and then pull it up while still putting pressure towards the front. The array should come up with the tool. When you see it, grab the array and pull it out of the unit.

If you cannot get the array out after doing this procedure, call technical support.

- 13. Put the hole plug back into the hole in the base piece of insulation.
- 14. Plug the scanner back in and turn it on.
- 15. Load the carousel after the scanner boots up.

If cartridges continue to become lodged in the AutoLoader, you should call technical support

GCS3000 with AutoLoader specification

Table 5 Item	Table 6 Parameter	Table 7 Value
Weight	Shipping	approx 115 pounds (52.2 Kg)
	Free-standing	approx 100 pounds (45.4 Kg)
Dimensions	Width	~13.25 in.
	Depth	~21.25 in.
	Height	~32 in.
Power	Voltage Current Line Frequency.	100 - 240 V ~ 4 - 2 A 50 - 60 Hz
Working Environment	Temperature	59°F-85°F (15°C-30°C)
	Humidity	10-90% Non- condensing
	Clearance	2 in. (5 cm) on side, back 12.5 in. on top
	Pollution Degree	2
	Installation Category	II
	Altitude	<2000m
Electrical Supply	Provide voltage, frequer unit label	ncy or power rating per
Main Supply Voltage Fluctuations	Are not to exceed $\pm 10\%$ voltage	6 of the nominal supply

GCS3000 with AutoLoader Specification Table

GeneChip[™] Command Console[™] (GCC) User Guide



Regulatory

This device complies with Part 15 of FCC Rules (Table 8). Operation is subject to the following two conditions: (1) This device may not cause harmful interference, and (2) This device must accept any interference received, including interference that may cause undesired operation.

This device complies with FDA performance standards for laser products except for deviations pursuant to Laser Notice No. 50, dated June 24, 2007.

This Class A digital apparatus meets all requirements of the Canadian Interference-Causing Equipment Regulation.

Cet appareil numérique de la classe A respecte toutes les exigences du Règlement sur le matériel broullier du Canada.

Regulatory Agency	Certification
CE	
Class 1 Laser Device	Complies with EN 60825-1:2007
	Complies with FDA performance standards for laser products except for deviations pursuant to Laser Notice No. 50, dated June 24, 2007
Hand held barcode reader is a Class 2 laser device	Complies with EN 60825-1:2007 Complies with FDA performance standards for laser products except for deviations pursuant to Laser Notice No. 50, dated June 24, 2007
	Compliant with directive 2002/96/EC (WEEE)

Table 8 Regulatory Certifications



Controlling the instruments

The GeneTitan MC instrument array plates need to be run through the following steps (within the array plate processing workflow), as shown in Figure 252.

- Hybridization
- Washing and Staining
- Imaging



GeneTitan array plates are processed using the GeneTitan Multi-Channel (MC) instrument, for genotyping and expression array plates.

There are differences in the workflows for genotyping array plates and expression array plates. This chapter describes the functions of GeneTitan Instrument Control that are common to both genotyping and expression array plates:

- "GCC GeneTitan instrument control software"
- "GCC GeneTitan scanner"
- "The GeneTitan MC instrument"
- "Overview of the GeneTitan workflow"
- "Tracking the array plate through the workflow"
- "Aborting a run"
- "Unload plates"
- "Using the wash-scan-resume workflow"
- "Using the wash only workflow"
- "Drop and scan with array plates"
- "Insufficient disk space notice"
- "Resetting the lamp life clock"
- "Computer practices, maintenance and troubleshooting"

Information specific to Expression Arrays is given in the Expression Assay Manuals.

Information specific to genotyping array plates is given in Axiom Genotyping Assay User Guide (P/N 702830).

See the GeneTitan Multi-Channel Instrument User's Guide (PN 08-0308) for a a detailed description of the instrument itself.

GCC GeneTitan instrument control software

The GCC GeneTitan Instrument Control software is used to control the GeneTitan Instruments.

Note: A computer used as a GeneTitan workstation requires a user account with specific privilege settings. In addition, some of the other features of Windows 10 Enterprise 2016 LTSB must be set up in particular ways or disabled to avoid causing problems when running GeneTitan IC software. The workstation is initially set up for use with GeneTitan has a default user account with these privileges and features already set.

IMPORTANT! If the GeneTitan workstation becomes unstable during a workflow the cost of an aborted workflow and replacement plates is substantial. To avoid this, it is recommended you Rebooting the instrument control computer weekly and follow the procedures described in "Computer practices, maintenance and troubleshooting".

Starting

1. Click the GCC GeneTitan Instrument Control icon in the GCC Launcher.

Click the Start \rightarrow Thermo Fisher Scientific \rightarrow Command Console GCC GeneTitan Control.

The GCC GeneTitan Instrument Control window opens.

See Figure 253 for 96 array plate GCC GeneTitan Instrument Control window example.



The software goes through the initialization process and starts the GeneTitan instrument.

You can track the initialization process in the Hybridization Oven Status pane (Figure 254).

After the initialization is completed, **System Ready** is displayed in the log, and you can display the Setup tab.

Figure notice	Figure 254 Hyb Oven log with System Ready notice									
	Hybridization Oven Status									
Position 1	tion 1 Barcode Estimated Time Remaining									
Position 2	Barcode Estimated Time Remaining									
- Oven Tem	perature									
Current	30 C									
Target	30 C									
9.27:10 AM 9.27:10 AM 9.27:10 AM 9.27:10 AM 9.27:10 AM 9.27:10 AM 9.27:10 AM 9.27:10 AM 9.27:11 AM 9.27:11 AM 9.27:11 AM 9.27:11 AM 9.27:23 AM 9.28:12 AM 9.28:12 AM 9.28:12 AM 9.28:12 AM 9.28:12 AM 9.28:12 AM 9.28:12 AM 9.29:27 AM 9.29:27 AM 9.29:27 AM 9.29:25 AM 9.29:25 AM	Log 9.27:10 AM OSVersion: Microsoft Windows NT 5.1.2600 Service Pack 3 9.27:10 AM UserName: AFFXUser 9.27:10 AM UserName: AFFXUser 9.27:10 AM ProductName: HT96CC 9.27:10 AM ProductName: HT96CC 9.27:10 AM ProductVersion96F : 3.0.0141 9.27:10 AM ProductVersion96F : 3.0.0141 9.27:10 AM ProductVersion965 canner: 3.0.0141 9.27:10 AM ProductVersion965 canner: 3.0.0141 9.27:10 AM ProductVersion965 canner: 3.0.0141 9.27:10 AM Destructure SPC: 6.023/2009 4:31:34 AM 9.27:10 AM ProductVersion965 canner: 3.0.0141 9.27:11 AM LastWrite Ime 956 canner: 6./23/2009 4:37:00 AM 9.27:11 AM McD & 965 files Copied: 19 9.27:11 AM LogFileDir set to: C:\Command_Console\Logs\96F 9.27:11 AM Homigh HT96F and Scanner. 9.27:23 AM Set HybD/ven temperature to 30 C. 9.27:23 AM Set HybD/ven temperature to 25 C. 9.28:12 AM Homing HT96F completed. 9.28:12 AM Seamner former drawer not extended or no plate present. 9.28:12 AM Seamner fonding completed. 9.28:12 AM Scanner forming completed. 9.29:27:34 M Checking and removing plate from scanner. 9.29:27:34 M Set Use Desch. 9.29:27:34 M Seamner forming completed. 9.29:27:34 M Second removing plate from scanner. 9.29:27:24 M Scanner forming completed for the scanner. 9.29:2									

The following notices may appear:

- Lamp Life setting (see "Resetting the lamp life clock")
- Insufficient Disk Space (See "Insufficient disk space notice")

Software components

- Menu bar: Provides access to IC functions.
- Tool bar: Provides buttons to access frequently used functions.
- System Setup/System Status tabs:
 - "System status window tab": Use to track the progress of array plates through the workflow.
 - "System setup window tab": Use to set up the GeneTitan Instrument for different workflows.
- Status bar and Progress bar: Displays information about the status of the GeneTitan Instrument and the workflow in progress.

Tool bar buttons

The **Stop** button is used to abort the array process. If there are two or more plates running in the instrument, the software will prompt you to select which process is to be aborted. See "Aborting a run".

The **Email** button opens the GCC Email Configuration File Editor, which enables you to send email messages about the instrument status. See Appendix E, "Notification emails" for more information.

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The Help button opens the GCC Online help file.

System status window tab

The System Status window tab (Figure 255) displays the progress of any currently loaded array plate(s) and features the following sections:

- Workflow
- Hybridization Oven Status
- Fluidics Status
- Imaging Device Status

The System Status tab is described in more detail in "Tracking the array plate through the workflow".

Figure 255 System Status window tab																			
File Tools Help																			
Stop Email Help																			
System Status Syst	em Setup																		
Work Flow																			
Barcode	Plate Type	Location	F	lyb. S	tatus	Flu	idics Status	Scan Status	Estimat	ed Con	pletion	Time	е						
5500944200216101714165	550094	Left Position	N	oActio	on	No.	Action	Completed	3/19/201	8 4:20:2	3 PM								
550094420021610171416	550094	Left Position	N	oActio	on	No.	Action	Running	3/20/201	8 1:32:0	ю РМ								
Estimated Time Windows	Pup Novt Hyb-Wash	Scon																	
Array Type	hate wee	rocali																	
3/20/2018 1:25:25 PM 3/20/	2018 1:29:07 PM																		
Hy	bridization Oven Statu	s		1			F	luidics Status				1						Imagi	ng Device
Dema de				Barc	ode							Ba	arcode			55009442	00216101	714165	-
Position 1			_	Prote	ocol Name							Estimated Time Remaining 00:09:35							
Estimated time to	maning			Estin	nated Time	Remainin	g					Lamp Life Remaining 63 hours							
Barcode				W	ash B Temp	erature						F	late Status	Log					
Estimated Time R	maining			Cu	urrent		32 C							1	2	3	4	5	6
Oven Temperature				l larget 32 C										-	-	-	-		
Current 27 C				Prot	tocol Log								► A						
Target 31 C					Step T	ask				Time	Status		в						
Log																			
4:00:54 PM HT96CC started at 4:00:54 PM MachineName: MC	3/19/2018 4:00:29 PM GTOWIN10IOT												c						
4:00:54 PM OSVersion: Microso 4:00:54 PM UserName: affxuse	ft Windows NT 6.2.9200.0												D						
4:00:54 PM ExecutablePath: C 4:00:54 PM ProductName: HTS	\Program Files (x86)\Affyme 6CC	etrix\Command Console\HT	T96(E						
4:00:54 PM Product Version 96F 4:00:54 PM Last Write Time 96F	3/19/2018 1:17:10 PM												_						
4:00:55 PM Product Version 965 4:00:55 PM Last Write Time 965	canner: 5.0.0.145 canner: 3/19/2018 1:15:27	PM											F						
4:00:55 PM C:\Program Files (x 4:00:55 PM GetLibraryPaths: C	36)\Affymetrix\Command Co \Command_Console\Libran	onsole\\GeneChipHTScan(y\	Con										G						
4:00:55 PM AuditLogDir set to: 4:00:55 PM LogEleDir set to: C	C:\Command_Console\Log C:\Command_Console\Log	s\96F													-	_			
4:00:55 PM Timer started with I 4:00:55 PM Homing HT96F and	terval: 1000 msec Scanner												н						
4:00:55 PM Set HybOven temp 4:00:55 PM Set WashB temper	erature to 31 C. ature to 32 C.																		
4:01:29 PM Homing H 196F completed. 4:01:29 PM Initializing Scanner.													Wil	Be Scanne	ed		w	I Not Be S	canned
4:01:29 PM Status: Scanner drawer not extended or no plate present. 4:02:59 PM Scanner homing completed. 4:02:59 PM Charling and serving plate from econner.													Nov	v Scanning			S So	an Comple	ited
4:02:59 PM Checking and remo 4:03:30 PM Status: No Plate in 4:02:23 PM Status: No Plate in											Total: 2				Will be Sc	anned: 0			
4:03:33 PM System Ready. 4:03:33 PM Lamp Life Remainin	g is 65 hours.																		
4:05:31 PM UniveC:\ tree space 4:05:31 PM Minimum free disk s	pace required is 1.5 GigaBy 144.0 GigaBytes	rtes																	
1:22:25 PM DriveC:\free space 1:22:25 PM Minimum free disk s	 144.0 GigaBytes pace required is 1.5 GigaBy 	rtes																	

System setup window tab

The System Setup tab is used to:

- Specify the type of workflow you want to perform.
- Enter a barcode for the array plate being processed.
- Unload and load trays and plates.
- Select arrays on the array plate for imaging.
- Upload data results to the Thermo Fisher Cloud.

Figure 2	256 System Setup	window tab	for genotyping	array plates		
GCC GeneTitan Instr File Tools Help Stop Email System Status	ument Centrol Føb System Stap					- 0 ×
Setup Option	Scan		System Layout		Array Selection	
Plate Information		Used Hyb Tray	Used Hyb Tray	Manual Array Selection		
Barcode	5500944200216101714165	Scan Tray	Scan Tray	1 2 3	4 5 6 7 8 9 10 1	12
Plate Type	550094	Stain 1 Tray	Ligation Tray	► A		
Protocol Name	550094.protocol	Stain 2 Tray	Stabilizing Tray			
1						
Location	Load consumables on left side	Stain 1 Tray		c		
Workflow Stepe		Array Plate	Hyb Tray			
onoiow ordps	Deved		Trash Bin	°		
Enter Array Plate Empty trash bin	Barcode			E		
Remove consum	nable trays and plates					
Load consumabl	le trays and plates			F		
Start Processing				G		
				н		
				Will Be Scanned	Will Not Be Scanned N	ot Available
					Thermo Fisher Cloud Settings	
				Connect To Cloud		
				Thermo Fisher Cloud User		
					user name accompany name.com	
				Thermo Fisher Cloud Upload Option	(A) Marrie (ADD //DC //CT)	
					Copy (ARR/JPG/CEL)	
				Thermo Fisher Cloud Folder	CytoScanProj	
				To upload data to	the Thermo Fisher Cloud, you must complete the information fields shown abo	ve.
Status						
Please select or	rays to scan using array selector					
i louse selectali	and a constant and a constant					
(Optional) To uple Cloud Settings" p check box.	oad data to the cloud, go to the "Thermo Fisher bane (lower right) and click the "Connect To Cloud"					
Press the Next bu	utton to advance to the next step.					
Cancel	Next					
Read barcode complet	ted.					

The System Setup window tab features four panes/sections:

- **System Setup:** Use to enter essential information and track progress of the setup and loading of the array plate and trays.
- **System Layout:** Indicates the drawers where different trays and array plates should be loaded. **Note:** The system layout changes based on whether Genotyping or Expression arrays are being processed.
- Array Selection: Enables you to select individual arrays on the array plate for imaging.
- Thermo Fisher Cloud Settings: Upload data results to the Thermo Fisher Cloud.

System setup

Figure 257	Setup Option pane										
Setup Option	Hyb-Wash-Scan]									
Plate Information											
Barcode	Barcode 55003201xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx										
Plate Type		Plata Information									
Protocol Name		Flate Information									
Location	Load consumables on left side										
Workflow Steps - Enter Array Plate Refill glass bottle Empty trash bin Remove consum Load consumabl Select arrays to a Start Processing	Location Load consumables on left side Workflow Steps Enter Array Plate Barcode Refill glass bottles with buffer Empty trash bin Remove consumable trays and plates Load consumable trays and plates Select arrays to scan Start Processing										
Status		1									
Please scan the Press the Next bu	Please scan the array plate barcode. Press the Next button to advance to the next step.										
Cancel	Next										

The Setup Option pane (Figure 257) has the following controls and displays:

Setup Options

[drop-down meu]

- Hyb-Wash-Scan
- Hyb-Wash
- Wash-Scan
- Wash-Scan-Resume

Select from the following workflow options:

- Wash Only
- Scan
- Unload Plates

See "Running a series of array plates" for more information.

Plate Information

Barcode	Barcode of the array plate.
Plate Type	Array Plate type.
Protocol Name	Name of protocol used for array plate processing.
Location	Side of drawer to load consumables.
Workflow Steps	Lists the steps to be performed during the operation.
Status	Displays information on the specific step to be performed, withThe plates and trays that need to be removed or placed.The drawer position the plates and trays should be place in.
Cancel	Cancels the setup.
Next	Proceeds to the next step (not displayed when performing a step that requires you to press the Confirmation button on the front of the instrument.

System layout

The System Layout pane (Figure 258) displays:

- Schematic view of the drawers to be loaded
- Indication of plate/tray position in drawer

Note: Different reagent trays are loaded when processing genotyping array plates and expression array plates. The correct trays are selected for display when the array barcode is entered, as shown in the figure below.



IMPORTANT! When running a series of array plates through the instrument, you must be careful to remove and load the proper array plate and trays and pay careful attention to the software prompts that tell you which side of the open drawer to remove or place a plate or tray.

Array selection



The Array Selection pane (Figure 259) displays the arrays to be scanned on the array plate:

- Manual array selection check box
- Plate Layout indicator, where you can:
 - Review the arrays available on the array plate.
 - Determine which are to be scanned.
 - Manually select arrays to be scanned on the plate. Note: By default, all arrays are selected for imaging.

The array selection process is described in the instructions for loading array plates in:

- Expression Assay Manuals
- Axiom Genotyping Assay User Guide (P/N 702830)



GCC GeneTitan scanner

1. Click Start \rightarrow Thermo Fisher Scientific \rightarrow GCC Launcher or double-click the GCC Launcher shortcut on the desktop.

The Launcher window appears. (Figure 260)

Figure 260 GCC Launcher menu - GCC Standalone Scanner Control
🖉 Launcher — 🗆 🗙
Command Console
GCC Portal
GCC Viewer
GCC GeneTitan Scanner
Tools
Thermo Fisher Cloud Administration
Gene Titan Library File Installer
Email Configuration Editor
Data Uploader
Resources
thermofisher.com
Support at thermofisher.com
Net Affx

Command Console

- GCC Portal (See "GCC portal home page")
- GCC Viewer (See Chapter 9, "Using the GCC viewer")
- GCC GeneTitan Scanner (See "Launching the scanner")

Tools

- Thermo Fisher Cloud Administration (See "Monitoring an instrument remotely")
- GeneTitan Library File Installer (See Appendix D, "Installing library files and scripts")
- Email Configuration Editor (See Appendix E, "Notification e-mails")
- Data Uploader (See "Scheduling auto-uploads")



- thermofisher.com (Home page)
- Support at thermofisher.com (Services and support page)
- NetAffx (Home page)

Launching the scanner

1. Click GCC GeneTitan Scanner.

The following window appears. (Figure 261)

Finune OCI Constitute Cooperate		
Figure 261 Gene I tan Scanner - Ma	ain window	
File View Tools Help Menu Bar		
Tool Bar System Setup		Live Image
Barcode Unknown		
Lamp Life Remaining 397h 22m		
Ime Remaining Unknown		
Will Be Imaged Will Not Be Imaged	Not Available	
Thermo Fisher Cloud Settings		
Connect To Cloud		
Themo Risher Cloud User	v	
Themo Risher Cloud Upload Option O Move (ARR/JPG/CEL)		
Copy (ARR/JPG/CEL)		
Themes Reher Cloud Folder		
Otatua Dar		Progress Bar
Ready. Status Bar		0

GeneTitan Scanner window options

- Menu bar: Provides access to the scanner functions.
- **Tool bar:** Provides the following buttons:
 - **Start**: Starts the scan process.
 - **Load**: Loads the plate into the scanner.
 - **X** = **Stop**: Aborts a scan in process.
 - Email: Opens the GCC Email Configuration File Editor. See Appendix E, "Notification e-mails" for more information.
 - **[?]** = **Help**: Opens on-line help.
- Barcode: Displays the barcode of the plate.
- Lamp Life Remaining: Remaining lamp life hours.
- **Time Remaining:** Time remaining until the plate is fully processed and complete.

- 8
- **Status and Progress bars:** Displays status of the GeneTitan instrument and the workflow in progress.

Using the scanner

1. Click the Start button.

After a few moments, its side door opens and a drawer slides out. (Figure 262)



A message appears (lower right) prompting you to place the plate onto the drawer.

2. Place the plate on the drawer making sure its orientation is correct (Figure 263) and the drawer's pegs match up correctly with the plate's bottom peg holes.



3. After placing the array plate onto the drawer (Figure 264), click the Load button.



The drawer retracts back into the scanner and the side door closes. After a few moments the barcode is detected and array pane populates, as shown in Figure 265.



Note: The following notices may appear:

- Lamp Life setting (refer to "Resetting the lamp life clock")



- 4. Click to select the wells you want to scan, as the **Manual Array Selection** check box is checked by default.
- 5. Optional: If you want to have your scanned data uploaded to the Thermo Fisher Cloud, click the **Connect To Cloud** check box now.

IMPORTANT! You cannot add a user(s) from the GCC Launcher \rightarrow Thermo Fisher Cloud Administration window (page 37) while the scanner application is open.

6. Click the Start button.

A message appears confirming if you want to continue.

7. Click **OK** to acknowledge the message.

After several minutes, the GeneTitan Scanner window populates, as shown Figure 266.

Fig	ure 26	6 0	aene	Titan	Scar	nner -	- pop	ulate	d exa	mple			
appliedbiosystems GeneTitan Scanner													
File Vi	File View Tools Help												
System Status													Live Image
Barcode	Barcode 55009411111111119988												
Lamp Li	Lamp Life Remaining 291h 45m												
Time Re	maining	07:10	:06										
	1 2		3	4	5	6	7	8	9	10	11	12	
	ç	c	c	c									
L' î	5	3	3	J									
в													
													2010 10 10 10 10 10 10 10 10 10 10 10 10
с													
D													
F													
F													
G													
н													
Will	Be Imaged			Will	Not Be Im	aged							
Nov	r Imaging			S Ima	ging Com	pleted			X	maging Fa	ailed		
Total: 96				Will be In	naged: 92				Imag	ed: 4			
	Thermo Fisher Cloud Settings												
Connect To Cloud													
Thermo	Fisher Cloud Use	r											
Thermo	Fisher Cloud Upl	oad Optio	n										
					C) Move (AF	RR/JPG/CE	L)					
					0) Copy (AR	R/JPG/CEL	-)					

Thermo Fisher cloud settings (optional)

IMPORTANT! To use this option, you must have a Thermo Fisher Cloud account. To register, see "Creating a cloud account".

Make sure you have added the appropriate user account(s), as detailed in "Adding users".

Thermo Fisher Cloud Settings are not applicable for the data registered on network data roots.

Figure 267 Thermo	Fisher Cloud Settings pane						
	Thermo Fisher Cloud Settings						
Connect To Cloud	V						
Thermo Fisher Cloud User	username@companyname.com						
Thermo Fisher Cloud Upload Option	Move (ARR/JPG/CEL) Copy (ARR/JPG/CEL)						
Thermo Fisher Cloud Folder	Cyto_Scan_Study						
To upload data to the Thermo Fisher Cloud, you must complete the information fields shown above.							

Do the following to upload your completed data to your Thermo Fisher Cloud account:

- 1. Click to check the **Connect To Cloud** check box.
- 2. From the drop-down list, select a Thermo Fisher Cloud User.
- 3. Select a Cloud upload option.
 - Move Uploads your files to the cloud. CEL and JPG files are removed from your local drive, while copies of ARR, DAT, and AUDIT files are retained. (Recommended)
 - **Copy** ARR, JPG, CEL, and AUDIT files are copied and uploaded to the cloud. The original files remain on your local drive.
- 4. Enter a name for your Cloud folder.
- 5. Click Next.

Your newly uploaded folder and data now resides on your cloud account's Data Connect web page (left pane/folder view), as shown in "Using the cloud to share data results".

The GeneTitan MC instrument

Overview

The GeneTitan MC instrument is designed to serve medium to high throughput customers. This system supports 16, 24, and 96-format high throughput array plates and will support future array plate formats. The system integrates a hybridization oven, a fluidics station, and an imaging device.

Refer to the GeneTitan Instrument User Guide (P/N 08-0296) for more information.

GeneTitan Multi-Channel (MC) instrument

The GeneTitan MC Instrument can process both Expression Arrays and Axiom Assay. The instrument uses an external 300W Xenon lamp and has multiple filters to provide stable, efficient, well-collimated, uniform illumination to the array, optimizing exposure time to minimize photo-bleaching effects and maximize throughput.



GeneTitan MC instrument controls and indicator lights

The figure below shows the location of the wash bottles, loading drawers, and other controls for the GeneTitan MC instrument.





WARNING! The bottles are pressurized in normal operation. Wait until you see the prompt that the buffer bottles have been de-pressurized before opening and refilling or emptying the bottles.

The GeneTitan Instrument uses the indicator lights and button below (Figure 270).



Confirmation button: Press after completing certain steps for instrument setup, like adding fluids or adding trays and plates.

The button flashes blue when a step is pending.

Instrument Status lights:

- Solid yellow initialing/homing system
- Solid Green processing/available to process
- Blinking green normal operation message box is displayed and requires user input
- Blinking yellow abnormal event informational message box requires user response

All power to the instrument is turned on when the GCC GeneTitan Control software is started and turned off when the software is shut down. The I/O switch on the front of the instrument is inoperative when the instrument is being controlled using the software.

IMPORTANT! Do not make use of I/O switch on instrument panel to start/stop instrument. Use the menu item in the software.

Refer to the GeneTitan MultiChannel Instrument User Guide (P/N 08-0305) for more information.



Overview of the GeneTitan workflow

Running an array plate through the GeneTitan workflow involves the following sets of steps:

- 1. Set up the Instrument:
 - a. Prepare plates and trays with samples and solutions, including buffer solutions.
 - b. Select type of workflow to be performed.
 - c. Select the Protocol, if required.
 - d. Refill Bottles.

IMPORTANT! Once bottles are refilled, ensure that bottle caps are on tight.

e. Remove used trays, plates and covers from the instrument.

2. Load new trays, plates and covers.

There are different procedures for the different array and workflow types:

- Expression Assay manuals
- Axiom Genome Wide Human Assay User Manual (P/N 702830)
- 3. Begin Array processing and track the array plate through the workflow.
- 4. Empty the instrument.

You can:

- Select only part of the overall processing workflow to run (see "Workflow options")
- Run a series of array plates through the workflow for high-throughput operation (see "Running a series of array plates")

Workflow options

w options There are three sets of steps performed by the GeneTitan Instrument for array plate processing:

- Hybridization
- Wash and Stain
- Imaging (Scan)

The software enables you to perform all of these steps, or to select an option that runs only some of the steps, as described below.

You can choose from:

Hyb-Wash-Scan

This workflow performs all the steps on the array being processed.

- Hybridization
- Wash and Stain
- Scan
- Hyb-Wash

The Hyb-Wash workflow enables you to bypass the Scan step, performing only:

- Hybridization
- Wash and Stain
- Wash-Scan

The Wash-Scan workflow enables you to bypass the Hybridization step, performing only:

- Wash and Stain
- Scan
- Wash-Scan-Resume

This enables you to resume an interrupted workflow at any point in the Wash stage. See "Using the wash-scan-resume workflow".

Scan

The Scan workflow performs the scan only.

Selecting different workflows

Figure 271 Selecting workflow								
System Status	System Setup							
Setup Option								
Plate Information	Hyb-Wash-Scan Hyb-Wash Wash-Scan							
Barcode	Wash-Scan Resume							
Plate Type	Unload Plates							
Protocol Name								
Location								

Selecting the different workflows may require loading the array plate on a different tray (array plate cover, hybridization tray, or scan tray). In addition, there are differences in how the workflows are performed on genotyping arrays and expression arrays.

These differences are detailed in:

- Expression Assay manuals
- Axiom Genotyping Assay User Guide (P/N 702830)

Differences in processing for genotyping and expression arrays There are instrumen • Geno

There are two types of Array Plates that can be processed using the GeneTitan instruments

- Genotyping array plates
- Expression array plates

Genotyping array plates

Genotyping Array Plates can be processed only on GeneTitan MC instruments, since they need to be scanned at two different wavelengths.

For genotyping arrays, the reagents trays need to be loaded twenty-four hours after the array plate and hybridization tray have been loaded, after hybridization has completed.

Needed reagents trays are:

- 2 each Stain1 trays with covers
- · Ligation tray with cover
- Stain 2 tray with cover

GeneChip[™] Command Console[™] (GCC) User Guide

- Stabilizing tray with cover
- Scan tray with holding buffer and cover

See the Axiom Genotyping Assay User Guide (P/N 702830), for more information on running genotyping array plates.

Expression array plates

Expression Array plates can be processed on a GeneTitan MC instrument.

Needed trays/reagents are:

- SAPE 1 Stain tray with cover
- AB Stain Tray with cover
- SAPE 2 Stain tray with cover
- · Scan tray with holding buffer and cover

See the Expression Assay manuals for more information.

Running a series of array plates

The GeneTitan Instrument can run two different workflows for the same probe array type at the same time. This enables you:

- To load a series of array plates with hyb trays and consumables for the Hyb-Wash-Scan workflow to process arrays more quickly.
- To run an array plate that was processed using a different system through the scan workflow while another array plate is going through earlier stages of the Hyb-Wash-Scan workflow.

Only certain types of workflows can be run at the same time, and delays may be necessary before starting the second workflow. These restrictions exist because an array plate should be scanned immediately after the wash and stain processing is finished, and GeneTitan scans one array plate at a time. In addition, there are restrictions caused by the differences in workflows for Axiom arrays and Expression arrays, and by differences in the number of arrays on the plates. For more information, see:

- Expression Assay manuals
- Axiom Genotyping Assay User Guide (P/N 702830)

Tracking the array plate through the workflow

You can review the progress of the Workflow in the System Status tab. (Figure 272)

Point Holp State Holp	Figure 272 GCC GeneTitan Contr	ol software, System Statu	s Tab	
Per Tosk Heig Store Store Store Store Marken Stare Store Marken Stare Store Store Store				
Web Row Batcada Plats Type Lackton Maining Valing \$2420301000000000000000000000000000000000	File Tools Help Stop Email Help System Status System Statup			
Hybridization Oven Status Fluidics Status Imaging Device Status Posten Bacode 5003201 xxxxxxxxxxxx Bacode Edmadd Time Remaining Bacode Posten Bacode Edmadd Time Remaining Dot 29:46 Bacode Edmadd Time Remaining Bacode Posten Bacode Edmadd Time Remaining Concent 26:7 C Concent 26:0 C Dot 10:0 C Dot	Work Flow Plate Type Location Hyb. Statu 55003201xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx	Fluidics Status Scan Status Estin Waiting Waiting 6/24/	sted Completion Time 009 10:48:16 AM	
Bacode 500301/scoccoccocco Pontion 1 Bacode Interded Time Remaining OC 29 : 46 Dention 2 Bacode Interded Time Remaining Stoccoccoccoccoccoccoccoccoccoccoccoccocc	Hybridization Oven Status	Fluidics Status		Imaging Device Status
Position 2 User of the memory status Particle 1 Parit 1 Particle 1 P	Position 1 Barcode 55003201xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx	Barcode Protocol Name Estimated Time Remaining	Barcode Estimated Time Remain Lamp Life Remaining	ning 59 hours - Warning: Low Lamp Life Remaining
1004183M TASK HijkoMoveToOverPosition1[55003201xxxxxxxxxxxx] pick 1004183M TASK HijkoMoveToOverPosition1[55003201xxxxxxxxxxxx] pick 1004120 M Retract Dravet6 100421 AM Gripper Does 100423 AM Retract Hybin	Estimated Time Remaining Current 30 Target 30 Target 30 Total State 1001:25 AM Gripper Date 100:25 AM Gripper Date 1001:25 AM Breact Haln 100:56 AM Gripper Date 1001:25 AM Breact Haln 100:20 AM HTA and sample plate combined: 55003201xxxxxxxxxxxx 100:20 ZM HTA and sample plate combined: 55003201xxxxxxxxxxxxx 100:20 ZM HTA and sample plate combined: 5003201xxxxxxxxxxxx 100:20 ZM HTA and sample plate combined: 5003201xxxxxxxxxxxxx 100:20 ZM HTA and sample plate combined: 5003201xxxxxxxxxxxx 100:20 ZM HTA and sample plate combined: 5003201xxxxxxxxxxxxx 100:20 ZM HTA and sample plate combined: 5003201xxxxxxxxxxxxx 100:20 ZM HTA and sample plate combined: 5003201xxxxxxxxxxxxx 100:20 ZM HTA and sample plate combined: 5003201xxxxxxxxxxxxxxxxxxxx 100:20 ZM HTA and sample plate combined: 5003201xxxxxxxxxxxxxxx 100:20 ZM HTA and sample plate combined: 5003201xxxxxxxxxxxxxx 100:20 ZM HTA and sample plate combined: 5003201xxxxxxxxxxxxx 100:20 ZM HTA and sample plate combined: 5003201xxxxxxxxxxxx 100:20 ZM HTA and sample plate combined: 5003201xxxxxxxxxxxxx 100:20 ZM HTA and sample plate combined: 5003201xxxxxxxxxxxxxx 100:20 ZM HTA and sample plate combined: 50003201xxxxxxxxxxxx 100:20 ZM HTA and sample plate combined: 50003201xxxxxxxxxxxxx <t< th=""><th>Current 26.7 C Target 25 C Protocol Log Step Task</th><th>Time Status</th><th>3 4 5 6 7 8 9 10 11 12 9 4 5 6 7 8 9 10 11 12 9 9 10 12</th></t<>	Current 26.7 C Target 25 C Protocol Log Step Task	Time Status	3 4 5 6 7 8 9 10 11 12 9 4 5 6 7 8 9 10 11 12 9 9 10 12
L'antes Dessin	100418 AM IASK Hyb/Move I oUverPosition [1500320] xxxxxxxxxxxxxxx pick 100418 AM Integer Core 100422 AM Retact Drawe6 100422 AM Ringer Core 100422 AM Ringer Core 100428 AM Retact Hybin 100428 AM Retact Hybin 100428 AM Retact Hybin 100428 AM Retact Hybin	Eludics Status	Scenner Status	#

It has the following sections:

- "Workflow status"
- "Hybridization status"
- "Fluidics status"
- "Imaging device status"

Workflow status The Workflow pane provides an overview of the array processing. (Figure 273)

Figure 273 Workflow pane							
Work Flow Barcode	Plate Type	Location	Hvh Status	Eluidics Status	Scan Status	Estimated Completion Time	
5500321234567890123456	550032	Left Position	Running	Waiting	Waiting	6/11/2009 6:58:00 PM	
Estimated Time Window to HT Array Type Same p	Run Next Hyb- late type	Wash-Scan	~				

The Work Flow table lists the array plates and their status in the workflow, with the following information:

- Barcode of array plates being processed
- Plate Type
- Location
- Hyb. Status
- Fluidics Status
- Scan Status
- Estimated Completion Time

Note: If more than three arrays are loaded at a time, a scroll bar appears at the right side of the table.

The Estimated Time Window information on when the next hyb-wash-scan workflow can be run

• Array Type

Note: You cannot select a different array type for the next array to be run.

• Time when you can load the next array plate and other consumables.

Note: When processing genotyping Arrays, once processing begins you have a specified period of time during which you can load another Array Plate and hyb tray. You cannot load another array plate before or after this period of time.

Hybridization status

The Hybridization Status pane displays details of the hybridization operations that have been run. The pane can display information for two array plates that are being processed at the same time.

Position 1	Barcode Estimated Time Remaining	
Position 1	Estimated Time Remaining	
Position 2		
Position 2	Barcode	
	Estimated Time Remaining	
Oven Temp	erature	
Current	30 C	
Target	30 C	
11:30:47 AM 11:30:47 AM 11:30:49 AM 11:30:49 AM 11:30:49 AM 11:30:49 AM 11:30:49 AM 11:30:49 AM 11:30:49 AM 11:30:49 AM	Product/version965camer: 30.01.25 Last/witeTime 95camer: 6:2/2005 MED & 95S files Expired: 26 Auditu.gDir set to: C:\Command_Con LogFieDir set to: C:\Command_Con LogFieDir set to: C:\Command_Con Timer started with Interval: 1000 mse Horning H195F and Scamer. Set WashB temperature to 30 C. Horning H195F completed. Initializing Scamer.	5 9 3:39:50 AM nsole\Logs\96F sole\Logs\96F sc
11:31:32 AM 11:31:33 AM	ScannerOff Option is on.	a
11:31:32 AM 11:31:33 AM 11:31:36 AM 11:31:36 AM	ScannerOff Option is on. Status: Scanner drawer not extender ScannerOn Option is on.	d or no plate present.

The pane displays the following information:

- Position 1
 - Barcode of the array plate(s) being processed
 - Time Remaining
- Position 2
 - Barcode
 - Time Remaining
- Oven Temperature
 - Current.
 - Yellow: Out of range
 - Green: In range
 - Target
- Log
 - Displays history of the operations performed in the Hybridization stage.

Fluidics status The Fluidics Status window (Figure 275) displays information on the wash and stain operations that have been run or are currently being run.

			Fluidics Status		
Barcode	,		550094p30000000000	***	
Protocol	Nam	ie	550094.protocol		
Estimate	d Tin	ne Remaining	00:00:00		
Wash Currer Targel	B Te ht	mperature 27 He	. 3 C ater is OFF		
Protoco	itep	og Task		Time	Status
1					
2					
3					
4					
5					
6					
7					
8					
9					
1)					
1					
1					
1					
1.					

The Fluidics Status window displays the following information:

- · Barcode of the array plate being processed
- Protocol Name
- Time Remaining
- Temperature for the protocol step
 - Current
 - Yellow: Out of range
 - Green: In range
 - Target
- Protocol tab:
 - Displays list of steps in the protocol with:
 - Step
 - Task: short description of the task
 - Time
 - Status: Task pending, in process, or completed?
- Log tab
 - Displays history of the operations performed in the Fluidics stage.

Imaging device status

The Imaging Device Status pane (Figure 276) displays the progress of the scan.

					Ima	iging	g De	vice	Stat	us			
rcod	e												
timat	ed T	ime F	Rema	ining									
mp L	ife R	lemai	ning		166	5 hou	IS						
ate S	tatu:	s L	og										
		1	2	3	4	5	6	7	8	9	10	11	12
•	A												
	В			2									
	С												
	D							_					
	E												
	F		_	2				-				-	_
	G	_		-	-	-	_	_	_	-			
	н												
	н	Re Sc	anneo	 1		YAL N	lot Be	Scann	ied				

The Imaging Device Status window displays:

- · Barcode of the array plate currently being scanned
- Time Remaining for scan
- Lamp Life/Imaging Device Status (see "Lamp Life/Imaging device status notices", below, for details)
- Plate Status tab with:
 - Array Plate Layout

Each square represents an array with the following options:

(Dark blue)	To be scanned
(Light blue)	Now imaging
(White)	Not to be scanned
Green	Scan completed
(Red)	Scan failed

• Log: displays history of the operations performed in the Fluidics stage. Lamp Life/Imaging device status notices

The Imaging Status pane displays lamp life and Imaging Device status notices for the GeneTitan MC.

In normal operation, the pane displays the hours of life left in the lamp:

Figure 277 Lamp Life above tolerance					
	Imaging Device Status				
Barcode					
Estimated Time Remaining					
Lamp Life Remaining	166 hours				

It displays a red or yellow notice when the lamp life is getting short:

Figure 278 La	mp Life above tolerance
	Imaging Device Status
Barcode	
Estimated Time Remaining	
Lamp Life Remaining	-1 hours Replace lamp as soon as possible

It also displays a red notice when the Imaging Device is offline:

Figure 279 Imaging Device Offline					
	Imaging Device Status				
Barcode					
Estimated Time Remaining	1				
Scanner Status	Offline: scanning is not available.				

Note: The 300 Watt Xenon lamp in the GeneTitan MC instrument is warranted for 500 hours. To replace the lamp refer to the instructions in the GeneTitan instrument manual. After changing the lamp, it is necessary to reset the lamp life clock manually. For more information about the clock, see "Resetting the lamp life clock".


Aborting a run

If necessary, you can abort a run in progress.

IMPORTANT! If you want to abort a run while loading reagents for a genotyping array plate, you must use the Cancel button in the tool bar. During reagent load the abort function will not be available for the plate for which reagent trays are being loaded.

For information on aborting a run because of facility power loss, see "Facility power loss" on page 254.

To abort a run:

1. Click the **Stop** button in the tool bar.

The Abort dialog box opens. (Figure 280)

Figu	Figure 280 Abort dialog box								
Plat	Plates Being Processed								
Se	Select Barcode Plate Type Location								
	~	550033	550033	Left Position					
Curr	rent S	itep							
Ple: P P	Please select Plate(s) to abort Press Abort button to abort Press Cancel button to cancel								
	Abort Cancel								

The Abort DB has the following components:

- Plates Being Processed List with the following columns:
 - Select check box
 - Barcode
 - Plate Type
 - Location
- Current Step: explains the next step in the procedure.
- Abort and Cancel buttons.
- 2. Click the Select check box for the plate whose run you want to abort.
- 3. Click Abort.

The software asks for confirmation.



Figure 281 Abort Confirmation						
Are you sure?						
<u>Y</u> es <u>N</u> o						

Click Yes to continue with the Abort process.

Note: The abort process may take some time to complete. Wait until it is finished before trying to perform any other operations.

When abort is completed, you can see the notice in the Status tab (Figure 282).

Figure 282 Abort notice in Workflow pane								
Work Flow								
Barcode	Plate Type	Location	Hyb. Status	Fluidics Status	Scan Status	Estimated Completion Time		
550033>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>	550033	Left Position	NoAction	NoAction 🤇	Aborted	6/23/2009 2:14:13 PM		
5500321xxxxxxxxxxxxxxx	550032	Left Position	Running	Waiting	Waiting	6/23/2009 7:36:18 PM		

If the array plate is in the Hyb Oven, it is placed in Drawer Number 1

If the array plate is in Fluidics when the abort is ordered, it is placed in the Scan tray.

You will need to unload the loaded plates and trays in a second step, using the Unload function or the unload steps during a setup.

Facility power loss

If facility power is lost and the UPS backup power battery percent remaining drops below 75%, the software will automatically abort all running plates. This automatic abort is intended to protect the plates by bringing all running plates out to the drawers for removal. However, if the user is in the setup tab performing setup steps (loading the machine) the software is prevented from performing the required abort sequence.

If facility power is lost and the user is notified that the UPS power percent remaining drops below 75%, the user should cancel the loading operation to initiate the abort sequence.

Canceling the loading operation and setup

• Select Cancel in the system setup tab.

Unload plates

The Unload Plates function can be used to empty the GeneTitan drawers after performing an abort operation.

Unloading loaded plates

1. Select Unload Plates from the Setup Option drop-down list. (Figure 283)

i gure 283 Se	electing workflow	
System Status	System Setup	
Setup Option		.
Plate Information	Hyb-Wash-Scan Hyb-Wash Work Scarr	ζ.
Barcode [Wash-Scan Resume	10/5
Plate Type	Unload Plates	
Protocol Name		-
Location		

The application prompts you to empty the cover trash bin.

- 2. Perform the following steps:
 - a. Open the trash bin door.
 - b. Remove and empty the trash bin.
 - c. Return the trash bin and close the door.
- 3. Press the **Confirmation** button to proceed.

The application prompts you to unload previously loaded plates and trays. For each loaded plate or tray:

• The appropriate drawer opens (Figure 284).



• The status box prompts you to remove the tray or plate and the system layout indicates the array or tray to remove. (Figure 285)



IMPORTANT! When running a series of array plates through the GeneTitan Instrument, you must be careful to remove and load the proper array plate and trays and pay careful attention to the software prompts that tell you which side of the open drawer to remove or place a plate or tray.

Figure 285 Unload trav(s)				
3 				
appliedbiosystems - GCC GeneTitan Instrument Control			- 0	×
File Tools Help				
🛛 🖾 ?				
Stop Email Help				
System Status System Setup				
Setup Option Unload Plates	×	System Layout	Array Selection	
Plate Information	Used Hyb Tray	Used Hyb Tray	Manual Array Selection	
Barcode	Scan Tray	Scan Tray		
Plate Type	Stain 1 Tray	Ligation Tray		
Protocol Name	Stain 2 Tray	Stabilizing Tray		
Location	Stain 1 Trav			
	Array Plate	Hvb Trav		
Workflow Steps		Trash Bin		
Empty trash bin				
Remove consumable bays and plates				
		╎╌╢╟║╢╠╾┼╌┼╌┼╌┼╌┼╌┼╌╢╟		
		╎╌║╽║╌┼╌┼╌┼╌┼╌┼╌╢		
		╎╴╞╢║┡╌╎╌╎╴╎╴╎╴╎╴╎╴╎	Thermo Fisher Cloud Settings	
			Connect To Cloud	-
			Thermo Fisher Cloud User	
		╎╌╡┠╎╏║┝╌╎╌╎╌╎╌╎╌╎╌╎╌╎╴╢╏	Themo Fisher Goud Upload Option	
			Copy (ARR/JPG/CEL)	
			Themo Either (Jourd Ender	
				_
			To upload data to the Thermo Fisher Cloud, you must complete the information fields shown above.	_
		\mathbf{N}		
Status	Plate	e/trav position and st	status indicators	
Remove the Scan Tray on Left side of Drawer.				
Remove the Scan Tray on Right side of Drawer.	-			
Press the Confirmation button when done.				
Cancel				
Drawer 2 opened.				

Remove any plate, plate receptacle, or tray from the drawer (Figure 285), then press the **Confirmation** button on the front of the instrument.

When you have finished emptying the old plates and trays, the software prompts you to proceed to the next step.



Using the wash-scan-resume workflow

The Wash-Scan-Resume can be used to resume an interrupted workflow on an array plate.

The Abort process places the Array Plate on the Scan Tray. **Note:** You must manually place the array on a blue tray before resuming the workflow.

Applied Biosystems recommends using a new scan tray for the resumed workflow.

Resuming an interrupted workflow

1. Select Wash-Scan-Resume in the setup process.

igure 286 Select OptionWash-Scan-Resume					
Set	up Option	Wash-Scan Resume			
Pla	ate Informatio	n			
B	arcode				
P	late Type				
P	rotocol Name				
L	ocation				

- 2. Enter the barcode for the interrupted array.
 - The Resume Plate dialog box appears.

Figure 287 Resume Plate dialog box						
Resume plate based on run history						
Resume place based on run history Image: Comparison of the place based on run history Plate: 55003201xxxxxxxxx Protocol: 550032.protocol Current step: 3 Status:NotStarted Current step: 3 Status:NotStarted Resume this plate's fluidic process starting from drawer 6, HTA plate on blue cover? Select YES to choose a starting step from unfinished steps remaining.						
Yes No						

The Resume Plate dialog box lists:

- Plate barcode
- Protocol that had been selected to run the array.
- Step where the process needs to be resumed.
- 3. Click Yes to proceed with the resume.

The ResumeStep dialog box opens.

Figure 288 Re	esumeStep dialog box
Select an unfir	nished step to resume fluidic processing
Step	
Step 2 WASHB NotS	tarted
Time to process at th	is step
0	seconds
Cannot exceed origin	al process time of 0 seconds
	Ok Cancel

The Steps drop-down list displays the uncompleted steps.

Figure 289 List of unfinished steps						
Select an unfinished step to I	resume fluidic processing					
Step						
Step 2 WASHB NotStarted	~					
Step 2 WASHB NotStarted	~					
Step 3 LIGATION NotStarted						
Step 5 STAIN1 NotStarted	=					
Step 6 WASHA NotStarted	_					
Step 7 STAIN2 NotStarted						
Step 8 WASHA NotStarted						
Step 9 STAIN3 NotStarted	<u>×</u>					

The list of unfinished steps are different for:

- Expression arrays versus Genotyping Arrays
- · Arrays interrupted in different parts of the workflow
- 4. Select the step in the workflow where you want to resume.

Note: If you have performed certain steps off-line, you need to skip these steps in the workflow.

5. Enter the time you want to run the first step in the Time to Process box.

You cannot change the processing time for certain steps, and cannot set the time to longer than the protocol specifies.

- 6. Click **OK** to resume the workflow.
- Follow the instructions in the software steps for loading the array and trays. You must load the array plate on a blue array base.



Thermo Fisher Scientific recommends using a new scan tray for the resumed workflow.

You must load all the trays for the original workflow; if you know you are going to skip a particular step, you can load an empty tray in the designated location for that step.

Using the wash only workflow

1. From the Setup Option drop-down menu, select Wash.

Figure 291	Select Option- Wash	
Colum Online	West	
Dioto Information	Wash	~
		-
Plate Type		-
Protocol Name		7
Location		

2. Click Next (bottom left).

The Barcode text field is enabled.

- 3. Enter a barcode.
- 4. Click Next.

The Workflow Steps pane populates, as shown in Figure 292.

Figure 292 Workflow Steps
W 14 0
Workflow Steps
Enter Array Plate Barcode
Refill glass bottles with buffer
Prepare WashB
Empty trash bin
Remove consumable trays and plates
Load consumable trays and plates
Start Processing

- 5. From the Protocol Name drop-down, select an appropriate protocol.
- 6. Click Next.

After a few moments, a Start Processing confirmation window appears. (Figure 293)

Figure 29	3 Start Processing	g confiri	mation	
IIII Start Proc	cessing	_		×
?	This will start the WashOn Please press the OK butto	ly in the Le n to confim	ft Position n.	
	ОК			

7. Click **OK**.

The Wash workflow begins.

Note: Monitor the Status pane as it continually updates the workflow's progress. Click **Next** when prompted. Completed workflow steps are highlighted in blue.

Drop and scan with array plates

While you can register an array plate and its arrays using the GCC Portal GeneTitan Array Plate Registration before processing, you can also process an array plate that has not been registered by using the Drop and Scan feature for array plates. When using Drop and Scan, the ARR, DAT, and CEL files for each array are named using the barcode and array position.

See "GeneTitan array plate registration" on page 135 for more information about registering an array plate.

Using Drop and Scan

- 1. Set up and load the GeneTitan Instrument as required for the workflow you are performing.
- 2. Process the array plate.

If the array plate has a valid barcode, it is processed and scanned. The ARR, DAT, and CEL files for each array are named using the barcode and array position and placed in the designated Default folder.

For more information about the Default folder, see:

- "Default folders"
- "Specifying a default folder"

If the instrument cannot read the barcode, or if there are no library files on the system for array plates with that part number, the array plate is ejected and an error notice appears.

Insufficient disk space notice

If there is not enough memory on the computer's drives to save the data from an array plate, a notice appears when:

- · You first initialize the software and instrument
- You select arrays for imaging.

Figure 294 Insufficient Disk Space Notice						
Barcode 5500321234567890123456	DriveID C	SpaceReqGB 12	FreeSpaceGB 311	PlateState Hyb	ScannerState Waiting	
DriveID FreeSpaceGB C 311	FreeSpa 299	ceRemainingGB	Status			
Insufficient disk space: Please free up sufficient disk space before scanning starts. You can check for sufficient disk space with the the menu command under Tools/Check Available Disk Space. Failure to do so will result in lost of data.						
			ок			

If you see this notice, you will need to free up sufficient disk space before imaging starts.



Resetting the lamp life clock

Note: The following resetting instructions can be used for either the GeneTitan or GeneTitan Scanner instrument.

The GeneTitan uses a xenon arc lamp system to provide illumination for imaging the array at two wavelengths. The xenon lamp has a limited lifetime and needs to be replaced at regular intervals.

The GeneTitan Instrument Control software provides a timer that indicates the remaining useful light of the bulb and notifies you when it requires replacement.

The replacement procedure is described in the GeneTitan Instrument User Guide (P/N 08-0296). After replacing the bulb, you will need to reset the time, as described below.

If life of bulb is under a specified limit, the following notice appears (Figure 295) when you launch the software:

Figure 295	Lamp Life Management notice
The Lamp Life Rema Lamp Life Remain Using the lamp be	ining is less than 60 hours. ing is 59 hours. yond the recommended time period will result in poor quality data.
Please exit the prog	ram and replace the lamp now.
If you have replace	d the lamp, please reset the counter for lamp life remaining.
Press OK to reset Press Cancel to s	the counter for lamp life remaining, kip reset.
	Cancel

If you click OK, the confirmation notice appears. (Figure 296)

Figure 296 Reset dialog box
Reset Counter for Lamp Life Remaining
Are you sure? Please make sure: 1. You had replaced the lamp before resetting the counter for lamp life remaining. 2. The lamp is plugged into an active socket and 3. The lamp power switch is in the ON position
Failure to replace the lamp will cause poor quality data. Failure to turn on the lamp will cause Scanner error.
<u>Y</u> es <u>N</u> o

Click **Yes** to reset the lamp life timer to the specified time.

Click No to cancel.

Computer practices, maintenance and troubleshooting

If the GeneTitan workstation becomes unstable during a workflow the cost of an aborted workflow and replacement plates is substantial. To avoid this Applied Biosystems recommends following certain computer operation practices and preventative maintenance routines.

These are described in:

- "Computer operation practices"
- "Preventative maintenance"
- "Troubleshooting"
- "Troubleshooting"

Computer operation practices

The following computer operation practices are recommended to help prevent problems.

Hard drive

For the instrument control system, it is recommended to keep all drives at a maximum of 50% full. If there is more data on the workstation, the system tends to slow down. If keeping data on the hard drives is absolutely necessary, the drives need to be defragmented regularly (ie: depending on the amount of data, every two weeks or monthly defragmentation is recommended).

USB memory drives/memory stick

When USB drives or memory stick(s) are connected to the workstation, please properly disconnect them (safely remove hardware) before physically pulling them off.

Scanning plates

If the GeneTitan system is scanning a plate or running fluidics, try not to run any other applications while the instrument workstation is running.

Moving data (DAT, CEL, etc.)

When archiving data or moving data off the workstation, it is highly recommended to do this process when scanning or running fluidics is not in process. The scanning process is very slow if data is being moved at the same time.

Preventative maintenance

Optimizing your disk drive

The drive(s) on the GeneTitan workstation need to be optimized regularly (ie: depending on the amount of data, every two weeks or monthly optimization is recommended).

- 1. Click the Search/magnifying glass icon (lower right).
- 2. In the Search Window text box, type defrag.
- 3. Click on **Defragment and Optimize Drives** selection. The Optimize Drives window appears.

Figure 297	Optimize Drives wi	ndow		
🁪 Optimize Drives			- 🗆 ×	
You can optimize you optimized. Only drive	ur drives to help your comput es on or connected to your co	ter run more efficiently, or omputer are shown.	analyze them to find out if they need to be	
Status —				-
Drive	Media type	Last run	Current status]
🟪 (C:)	Hard disk drive	2/26/2018 4:57 PM	OK (0% fragmented)	
DATAPART1 (D:)	Hard disk drive	3/26/2018 7:05 PM	OK (0% fragmented)	
- OS (E:)	Hard disk drive	3/26/2018 7:05 PM	OK (0% fragmented)	
🖋 (F:)	Removable drive	Never run	Optimization not available	
👝 (G:)	Removable drive	Never run	Optimization not available	
📻 (H:)	Hard disk drive	3/26/2018 7:05 PM	OK (0% fragmented)	
	Used disk drive	2/26/2010 7.05 DM	OK (0% fragmented)	
			Second Analyze Optimize	l
Scheduled optimizati	ion			-
On			😌 Change settings	
Drives are being	optimized automatically.			·
Frequency: Week	dy			
	-			

The window displays a list of drives with information about capacity and free space.

- 4. Select the disk you want to optimize.
- 5. Click Analyze.

The Analyze process runs.

When the analyzing process is complete, the status of your analyzed drive is displayed in the Current Status column.

Repeat steps 4-5 for each drive you want to optimize.

6. Close the Optimize Drives window.

Troubleshooting If the GeneTitan IC window and taskbar icon disappear

The GeneTitan IC window may disappear from the computer screen while, at the same time, the Taskbar icon for GeneTitan IC disappears. If this happens, restore the window and icon by doing one of the following.

Solution 1

1. Simultaneously press Ctrl/Alt/Delete keys.

The Windows Security dialog box appears.

2. Click Start Task Manager.

The Windows Task Manager window appears.

3. Click New Task...

The Create New Task dialog box appears. (Figure 298)

Figure	298 Create New Task dialog box
🖅 Create	e New Task
	Type the name of a program, folder, document, or Internet resource, and Windows will open it for you.
Open:	explorer.exe 🔻
	😵 This task will be created with administrative privileges.
	OK Cancel Browse

4. Enter explorer.exe and click OK.

The Task Bar should be displayed

5. Press the icon for GeneTitan in the task bar to display the GeneTitan window.

Note: The **explorer.exe** application must be running properly to display the Taskbar at the bottom of the screen. The above procedure will launch explorer.exe to re-display the Taskbar.

Solution 2

1. Simultaneously press the Alt and Tab keys

A list of icons for active applications appears.

- 2. Keep pressing the Alt key while tapping on the Tab key to select the window displaying GeneTitan.
- 3. When selected, release the Alt key.

The GeneTitan window re-appears.

Note: For more troubleshooting information, see the GeneTitan Instrument User Guide (P/N 08-0296) or GeneTitan Multi-Channel Instrument User Guide (P/N 08-



0305)



Using the GCC viewer

After the array has been scanned, GCC: (Figure 299)

- Aligns a grid on the Image (DAT) file to identify the probe cells.
- Computes the probe cell intensity data for the array and creates a CEL file.



The GCC Viewer displays DAT, CEL, and JPG files and enables you to:

- Track the progress of the data through grid alignment and cell intensity generation.
- View the files for quality control purposes, such as detecting scratches and bubbles.
- Check the grid alignment and realign the grid, if necessary. See "Checking the grid alignment" on page 310.

Note: Realigning the grids will update DAT headers and break the parent-child relationship between DAT files and existing CEL files until the CEL files are regenerated.

• Create a JPG version of a DAT file for archiving.

See "Exporting images in other formats" on page 322.

This chapter describes the operation of the GCC Viewer in the following sections:

- "Array and grid types", below
- "Introduction to the viewer" on page 275
- "Using the review window" on page 283
- "Opening image files" on page 289
- "Using the review window" on page 283
- "Learning about the image file" on page 307
- "Checking the grid alignment" on page 310
- "Exporting images in other formats" on page 322

Array and grid types

The Alignment algorithm uses the checkerboard image of the control probes, located at the corners of the probe array, to superimpose a grid on the scan image. The algorithm aligns the grid so that each square in the grid delineates a probe cell.

The alignment of the grid and sub-grids usually takes place automatically after imaging the array. The status of the alignment can be tracked in the Review window. If the alignment algorithm fails you can perform a manual alignment of the main grid and/or sub-grids.

Different types of arrays use different grid types, as described in:

- "Cartridge arrays"
- "GeneTitan array plates" on page 271

Cartridge arrays

Cartridge Arrays can use:

• Main Grid Only (Figure 300)

	ole Viewer							
File View Help								
🚰 Search & Open	🚰 Open File 📙 Sa	ve 🛛 🕜 Help						
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Arrau Information	•				• +	• (.•.).)	(*)	-
Array ID	042120a2-8cdb-4ca0-							
Array Name	@5106810024753001	08 =		10.12				
Barcode	@5106810024753001							
Design Type	Expression							
Probe Array Type	HG-U133A				and the second			
Sample File Name	C:\Command Console	vc III						
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						Alter Alter	dis the set	
Fluidics Date								
Fluidics Date Fluidics Module ID						La de Caller de Caller		
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Fludics Uate Fluidics Module ID Fluidics Module Nut Fluidics Station ID Fluidice Station Nut Arids	nt بل kctive Grid الله الله ش Image Processing م	×						
Fladice Ude E Fladice Module ID Fladice Module No Fladice Station Mu Gride Full Image H Full Image H Full Image H Workflow Review	다 Letive Grid 」 即 課題 第 印 Image Processing ㆍ	×						
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Volkflow Review Volkflow Review Refersh Sh	nt ketive Grid	7) Days 73 Name 75 106510024	(Apply)		s Only Fil Arrey Type HG-U132	ter by: Date Sc Scan Status Sran Status	canned 💌	P mer
Voikflow Review Workflow Review Workflow Review Workflow States	at tetive Grid The	7 Days ray Name 5106810024	Apply	Show Error 015385008	s Only Fil Array Type HG-U133A HG-U133A	lter by: Date Sc Scan Status Finished Finished	anned 💌	₽ mer

• Main Grid with multiple sub-grids (Figure 301)

The position of each sub-grid can be adjusted independent of the other sub-grids.

			_				
<u>Eile View H</u> elp							
🚰 Search & Open 🛛 🞽 O	pen File 🔛 Save	🕜 Help					
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					0 <	><	> 3015
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Probe Array Type Gen	omeWideSNP_6	Page 1		A STATE OF STATE	A State of the	and the state	
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Fluidics Station Num		a second		and the second	a destruction of	a log al log	here at the
Fluidics Status			Contractor inter				100 C
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	Age Processing •						
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Workflow Review	nage Processing •	7 Days Appl Well Positi.	y Chray Name	v Errors Only	Filter by: Da	ite Scanned 🕞	4 CEL Genera
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Each sub-grid is identified by its row and column in the main grid. The corners of each sub-grid are marked on the array by specific alignment patterns; the anchors of the sub-grid are aligned to these patterns. (Figure 302)



The software uses the corner patterns at the four corners of the array to align the initial main grid. The main grid is then divided into smaller sub-grids. Each sub-grid is aligned on the corner grid patterns in the final steps of the gridding algorithm and in manual alignment.

GeneTitan array plates

Plate Arrays use:

• Sub-grids only without a main grid (Figure 303)

There are two different types of Genetitan array plates:

- "GeneTitan expression array plates" on page 272
- "GeneTitan genotyping array plates" on page 275

GeneTitan expression array plates

🖏 Command Console Viewer	
File View Help	
🚰 Search & Open 🔎 Open File 🔙 Sa	ave 🕜 Help
Properties 4	× 550001_Tests_(HT_HG-U133A)_A07.DAT 4
2↓ 📼	
Array Information	
Array ID c0ff0518-e1fd-4ce8-ab	
Array Name	
Barcode 550001_Tests	
Design Type Expression	
Probe Array Type HT_Hts-UT33A Sampla File Mama	
Fluidics	
Fluidics Actual Time	
Fluidics Serial Numb	
Fluidics Wash B Ma:	
Fluidics Wash B Min	
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and Algonania versic 2.0.0.335	
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An array plate can have up to 96 arrays (see "GeneTitan array plate registration" on page 135 for more information).

Each plate array on the array plate has multiple sub-grids. Some arrays use a 7 x 7 grid, for a total of 49 sub-grids, while other array types use a 7 x 6 grid, for a total of 42 sub-grids.

These sub-grids are similar to the sub-grids used for some cartridge arrays, but on a plate array the sub-grids are not aligned to a main grid.

In addition, the data for all the mini-DAT files is consolidated into a single DAT file. This DAT file can be viewed in the Image Viewer; the file has all the image and gridding data for each sub-grid and each exposure, and enables you to check the gridding independently for each exposure



Figure 304 Mini-DAT and mini-CEL files

Relationship between plate arrays, Mini-DAT files, Mini-CEL files, and DAT files



Plate Array with subgrids

A plate array does not have a main grid, but has up to 49 independent subgrids.

Mini-DAT files

The array is scanned twice with different exposure times. Each scan produces a mini-DAT file for each subgrid, for a total of up to 98 different mini-DAT files





DAT file



The data for all the mini-DAT files is consolidated into a single DAT file. You can use the DAT file to view the individual subgrids for each exposure and to correct problems with Gridding

The data from each exposure is used to determine the cell intensity data for each subgrid. This data is kept in a mini-CEL file. In this example, there would be 98 mini-CEL files for an array, with two mini-CEL files for each subgrid.



The mini-CEL files for each exposure are merged into a single merged CEL file (.mgcel) (Figure 305), resulting in two merged CEL files per plate array.

The data in these two merged CEL files is then consolidated in a single CEL file, which is used for further analysis and can be viewed in the Image Viewer for QC purposes.



Figure 305 Mini-CEL merge and consolidation.



The mini-DAT files, mini-CEL files and merged CEL files will be deleted during normal processing. If something goes wrong, you may find these file types in the target folder during a scan.

GeneTitan genotyping array plates

GeneTitan genotyping array plates are handled similarly to the GeneTitan Expression arrays except that the arrays are scanned at two different wavelengths to support the two color assay. At each wavelength genotyping arrays are scanned at two different exposure times where signals from all four DAT files are integrated into a single DAT file to provide an expanded dynamic range.

Introduction to the viewer

You can learn more about the basic functions of the GCC Viewer in:

- "Opening the viewer"
- "File display differences" on page 276
- "Moving the components out of the viewer" on page 278
- "Moving the component borders in the GCC viewer" on page 281

Opening the viewer

To start the GCC Viewer:

 In the GCC Launcher, click the GCC Viewer icon <a>[]; or Click the Start → Thermo Fisher Scientific → GCC Viewer. The viewer opens. (Figure 306)

Figure 306 GCC Viewer w	ith no image displayed
Viewer menu	S Command Console Viewer
	File View Help
Viewer tool bar	🕺 🏂 Search & Open 🚰 Open File 🔙 Save 🛛 🔞 Help
	Workflow Hevrew
	Date Scanned Barcode Well Positi. Array Name A
	5/5/2011 4:50:11 PM @51059900309137041705400091668901 BAT_25 1 5/5/2011 4:41:22 PM @51133200123456101006123456712302 @51133200123456101006123456712302 1
	5/2011 1:57:24 PM @51068100247530010804300015385007 @51068100247530010804300015385007 + 5/5/2011 1:57:24 PM @51068100247530010804300015385009 @51068100247530010804300015385009 +
Review window	5/5/2011 1:53:41 PM @51068100247530010804300015385008 @51068100247530010804300015385008 5/5/2011 4:04:49 PM @51068100247530010804300015385008 @51068100247530010804300015385008
	5/3/2011 3:48:45 PM @51068100247530010804300015385008 @51068100247530010804300015385008 + 5/3/2011 3:11:14 PM @51068100247530010804300015385008 @51068100247530010804300015385008 +
Status bar	Cell X = 724, Cell Y = 0, Intensity = 2123

The viewer has the following components when it first opens:

- Viewer menu
- Viewer tool bar
- Review window (optional) (see "Using the review window" on page 283)
- Status bar: displays cursor position and intensity of selected pixel/cell

Additional components are visible when a DAT or CEL file is displayed (Figure 307)

Figure 307 Parts of the G	GCC Viewer with DAT file displayed
Viewer menu 🔍	🔍 Command Console Viewer
Viewer tool bar	Ele Yew Help Search & Open Sove W Help Properties # X INA06993_SH_050707_VM_SNP6_Plate1_D04_2.DAT 4 b ×
Properties box	Aray Information Aray Name Bacode Design Type Probe Aray Type GenomeWideSNP_6 Sample Fine Name Fluidices Pluidices Pluidices
Grid box	Gids Image Image <
Review window	Refesh Show Workflows of last: 7 Days Apply Show Errors Only Filter by: Date Scanned Date Scanned Barcode Well Positi. Array Name Array Type Scan Status Grid Alignment CEL Genera 5/5/2011 311:14 PM @5106810. @5106810. @5106810. Finished
Cursor position	Pixel X = 15066, Pixel Y = 0, Intensity = 256

To learn about the Image window tool bar, see "Changing the display of the image" on page 299.

To learn about the Properties box, see "Learning about the image file" on page 307.

To learn about the Grid box, see "Checking the grid alignment" on page 310.

File display differences

The GCC Viewer has different types of functions and options for the different image file types that it displays:

DAT files

DAT files are the image data files, the product of the initial scan. They are used to generate the cell intensity data file after the grid has been aligned.

The DAT file must be opened to perform manual gridding or to run the grid alignment algorithm in the GCC Viewer.



If the cell intensity data (CEL) file has been generated, you can click the **Cell Intensity** button and view the cell intensity data in the DAT Image window.

GeneTitan expression array plate DAT file exposures

Each array is scanned twice, with different exposure times. The image data from both exposures are in the GeneTitan Array Plate DAT file. You can switch between the different exposures for checking the gridding, etc., by using the Exposure button (see "Displaying different exposures (GeneTitan expression array plate DAT files only)" on page 303).

GeneTitan MC Genotyping Array Plate DAT File Exposures

In GeneTitan MC each array is scanned twice, with different colors. The image data from both exposures are in the GeneTitan MC Array Plate DAT file. You can switch between the different exposures for checking the gridding, etc., by using the Exposure button (see "Displaying different exposures (GeneTitan expression array plate DAT files only)" on page 303).

CEL files

CEL files are cell intensity data files, produced using the DAT file data after gridding and feature extraction.

You cannot perform grid alignment or cell generation on a CEL file.

For certain types of probe arrays, failed control features in the array will be masked when viewing the cell intensity data (see "Viewing failed control features", below).

JPG files

JPG files are a copy of the DAT image in a standard image file format; they provide an image file with a reduced file size for QC inspection, archiving, and publication.

Viewing failed control features

For certain types of probe arrays, the cell intensity analysis also generates a Cell Summary Report. The report has information on the control features on the array that failed certain quality checks.

The failed control features are masked when viewing the cell intensity data in these cases (Figure 308).



See "Changing the grid and intensity display" on page 302 for more information about controlling the grid and intensity display.

See Appendix C, "Cell summary report" on page 353 for more information about the cell summary report.

Moving the components out of the viewer

You can move the following components to a different location on your screen by clicking in the title bar and dragging the box to the new location (Figure 309).

- Properties box
- Grid box
- Review window



You can move the Image window outside of the Viewer by clicking on the file name tab and dragging the window out of the viewer.

Docking the boxes back in the GCC Viewer

1. Double-click on the box title bar or the file name tab in the Image window.

Choosing a new location for the bo

 Click on the title bar and drag the box back into the GCC Viewer. The docking hints buttons appear in the Viewer. (Figure 310)



2. Move the Cursor to the docking hint button.

A gray box appears, showing where the box will dock.

3. Release the mouse button.

The box is docked in the selected location. The title bar contains two options for the Properties and Grid boxes, Close and AutoHide. (Figure 311)

Figure 311	Box title bars	
Grids	р	x

Closing a box

1. Click the Close 🗙 button.

Using the Autohide feature

1. Click the **AutoHide** button **I** in the box.

The box is closed, but a tab is displayed on the left side of the window (Figure 312).

Figure 312 Hidden G	Grid Box and tal	o		
	<u>File H</u> elp			
	🕴 🚰 Open File 🛛 🚽	iave 🕜 Help		
Hidden Grid	Properties	- ÷ ×	HG-U133BC.DAT 4	$\triangleright \mathbf{x}$
-	2 ↓ 🖾		2, 🔍 🔲 📀 🕦 🛛 🔹 💽	=
	🖻 🗆 Array			
	ArrayBarcode	@5105562222333111805		
	Arrayld	HG-U133BC		
	ArrayType	HG-U133B		encerte.
	🗆 File		ATTACTOR STREET, STORAGE STREET	
	FileName	C:\Program Files\Affymetrix		
	FileSize	57832416		
	L and M and G and	4437730000 A-30.40 DM		10000

Displaying a hidden box temporarily

1. Place your cursor on the tab.

Restoring a hidden box

1. Display the box and click on the **AutoHide** button **I**.

Moving the component borders in the GCC viewer

You can change the relative size of a component in the Viewer by moving the borders of that component.

Changing the size of the component

1. Move the cursor over the border until it changes to a double arrow \Leftrightarrow .

File View Help		
Search & Open 🎯 Open File 🗔 Save	Ø Help	
Properties 📮 🗙	550001 Tests (HT HG-U133A) A07.DAT	4 Þ
12.2↓ □		0
Array ID c0ff0518-e1fd-4ce8-abr		
Array Name		
Barcode 550001 Tests		
Design Type Expression		
Probe Array Type HT HG-U133A		
Sample File Name		
Fluidics		
Fluidics Actual Time		
Fluidics Serial Numb		
Fluidics Wash B Ma:		
Fluidics Wash B Min		
Fluidics Wash B Set		
Grid Alignment		
Grid Algorithm Versic 2.0.0.993		
Grid Corners (244, 81), (1129, 89), (1		
Grid Status Auto aligned 🔛	Cursor on	
àrids 🕂 🕂 🛪 🗙	Ourson on .	
Full Image 🗰 Active Grid 🛛 💽 📴 🔤		
	· · · · · · · · · · · · · · · · · · ·	
- Image Processing -		
8		
/orkflow Review		ų
Refresh Show Workflows of last: 20	Days Apply Show Errors Only Filter by: Date Scanned -	
Date Scanned - Barcode	Well Positi Array Name	Array
5/5/2011 4:50:11 PM @51059900309	137041705400091668901 BAT_25	Test
5/5/2011 4:41:22 PM @51133200123	456101006123456712302 @51133200123456101006123456712302	True
5/5/2011 1:57:24 PM @51068100247	/530010804300015385007 @51068100247530010804300015385007	HG-L
5/5/2011 1:55:45 PM @51068100247	530010804300015385009 @51068100247530010804300015385009	HG-L
5/5/2011 1:53:41 PM @51068100247	530010804300015385008 @51068100247530010804300015385008	HG-U

2. Click and drag the cursor to change the size of the area (Figure 314).

Figure 314 Grid box enlarged.	
File View Help	
Search & Onen Ele Save M Heln	
	4
Array Name	
Barcode 550001_Tests	
Design Type Expression	10.00
Probe Array 1996 Hi - HG-U133A	
Grids 🕂 🛪	1.1
Full Image 🔛 Active Grid 🛛 🛃 🎆 🎆	
🕐 🖓 👝 🙀 🛱 Image Processing 👻	
	100
	6.27
	1.1.1
	1.1
	÷
	_
Workflow Review	. x
A Bafreeh Show Workflows of last 20 Dave (Apply) Show Errors Only Filter by: Date Scanned -	
Therean Condwinter of the Condwine Cond	_
Date Scanned Vell Positi Array Name	Array
Solution + 30, 11 PM (e510330030913704170040001666301 BAT_20 Solution + 30, 11 PM (e51133200123456101006123456712302 (e51133200123456101006123456712302	True
5/5/2011 1:57:24 PM @51068100247530010804300015385007 @51068100247530010804300015385007	HG-L
5/5/2011 1:55:45 PM @51068100247530010804300015385009 @51068100247530010804300015385009	HG-L
Control 1:03:41 PM @51068100247530010804300015385008 @51068100247530010804300015385008 @51068100247530010804300015385008	HG-L
	2
Pixel X = 140, Pixel Y = 858, Intensity = 25	:

Using the review window

The Review window, at the bottom of the viewer (Figure 315), displays a list of DAT files for scanned arrays. The window includes various information on the DAT files, including the grid alignment and cell generation status.

Figure 315	Review window									
	Workflow Review									д X
Toolbar	🥏 Refresh 📗 Show Wo	rkflows of last: 7	Days Apply	Show	Errors Only	Filter by: Da	te Scanned 🔹		Number of Record(s): 8
	Date Scanned	▲ Barcode \	Vell Positi Arra	y Name	Array Type	Scan Status	Grid Alignment	CEL Generation	Date Reviewed	Err
	5/3/2011 3:11:14 PM	@5106810	@5	106810	HG-U133A	Finished	Finished	Finished	5/5/2011 3:26:54 PM	~
	o 5/3/2011 3:48:45 PM	@5106810	@5	106810	HG-U133A	Finished	Finished	Finished		
	🧕 5/3/2011 4:04:49 PM	@5106810	@5	106810	HG-U133A	Finished	Finished	Finished		=
	🧿 5/5/2011 1:53:41 PM	@5106810	@5	106810	HG-U133A	Finished	Finished	Finished	5/9/2011 11:12:30 AM	
	🧕 5/5/2011 1:55:45 PM	@5106810	@5	106810	HG-U133A	Finished	Finished	Finished	5/9/2011 11:09:48 AM	
	🥝 5/5/2011 1:57:24 PM	@5106810	@5	106810	HG-U133A	Finished	Finished	Finished		~
	<		1111							>

The Toolbar provides access to different functions of the window.

The Review window displays a list of the scans performed along with the following information:

Status Icon	In progress.
	Finished
	S Failed
Date Scanned	Date and time the array was scanned.
Barcode	Array Barcode.
Well Position	Well Position for Array Plate.
Array Name	Name of the array file created.
Array Type	Probe array model scanned.
Scan Status	Status of scan.
Grid Alignment	Status of grid alignment.
CEL Generation	Status of cell file (CEL) generation.

Date Reviewed Data and time the DAT file was last viewed in the Viewer.

Error Message Short message describing the error found [do we need list of codes?].

	Error Message	DAT File Name	CEL File Name
	GridAlignment.exe: Failed	@51133200123456101006123456712302_2_A.DAT,	@51133200123456101006123456
-		BAT_25.DAT	BAT_25.CEL
l	GridAlignment.exe: Failed	@51133200123456101006123456712302_A.DAT, @5	@51133200123456101006123456
	4	BAT 25 3.DAT	BAT 25 3.CEL
	Grid/ <mark>GridAlignment.exe: Fai</mark> GridAlignment.exe: Fai	led to find checkerboard patterns that may be confused with led to find checkerboard patterns that may be confused with	the corner checkerboard pattern. the corner checkerboard pattern.
		@51068100247530010804300015385008_5.DAT	@51068100247530010804300015
		@51068100247530010804300015385008_4.DAT	@51068100247530010804300015
Mo	ouse over the error	r message to see a popup of the en	tire message.

DAT File Name Name of the DAT file(s) generated.

DAT File Name	CEL File Name
@51133200123456101006123456712302_2_A.DAT,	@51133200123456101006123456712302_2_A.
BAT_25.DAT	BAT_25.CEL
@51133200123456101006123456712302_A.DAT, @5	@51133200123456101006123456712302_A.CE
BAT_25_3.DAT	BAT_25_3.CEL
@51133200123456101006123456712302_3_A.DAT,	
BAT_25_2.DAT	BAT_25_2.CEL
@510681Q0247530010804300015385008_5.DAT	@51068100247530010804300015385008_5.CE
@5106810247530010804300015385008 A DAT	@51068100247530010804300015385008_4.CE
@51068C:\Command_Console\Data\Default\@51068100	247530010804300015385008_5.DAT 385008_3.CE
@51068100247530010804300015385007.DAT	@51068100247530010804300015385007.CEL
Mouse over the DAT file name to se	a tha full path

Mouse over the DAT file name to see the full path.

CEL File Name Name of the CEL file(s) generated.

Г

CEL File Name	Last Updated
@51133200123456101006123456712302_2_A.CEL, @	5/15/2011 11:14:24 AM
BAT_25.CEL	5/5/2011 4:50:11 PM
. @51133200123456101006123456712302_A.CEL, @51	5/5/2011 4:41:22 PM
BAT_25_3.CEL	5/15/2011 11:19:10 AM
	5/15/2011 11:17:43 AM
BAT_25_2.CEL	5/15/2011 11:16:11 AM
@51968100247530010804300015385008_5.CEL	5/3/2011 4:04:49 PM
@51058100247530010804300015385008_4_CEL	5/3/2011 3·48·45 PM
@5 C:\Command_Console\Data\Default\@510681002475	30010804300015385008_5.CEL
@51068100247530010804300015385007.CEL	5/5/2011 1:57:24 PM
Mouse over the CEL file name to see	the full path.

Last Updated Date the workflow last ran.

Enable or disable the Review window

1. From the View menu, select **Review Window**.

The Review window displays a list of the scanned arrays with their DAT files and their grid alignment and cell generation status.

Displaying a listed DAT file

1. Double-click on the file in the list.

If the workflow is associated with more than one DAT file, the Choose File to Open dialog box opens (Figure 316).

Figure 3	16 Choose File to Open dialog box
Choose File	To Open 🛛 🔀
Files Path:	C:\Command_Console\Data\Default
05110000	
@51133200	0123456101006123456712302_A.DA1 (Auto aligned) 0123456101006123456712302_B.DAT (Not aligned)
@51133200 @51133200	0123456101006123456712302_C.DAT (Not aligned) 0123456101006123456712302_D.DAT (Auto aligned)
	<u> </u>

• Select the DAT file to open and click the **OK** button in the Choose File to Open dialog box.

The image file is displayed in the viewer. (Figure 317)

File View Help						
nie view nietp						
5 Search & Open 🦾 Ope	n File 🔚 Save 🛛 🔮	Help				
operties	д X	BAT_25.DAT				4
2↓ 🖾	11	🛪 🔍 🔍 🔍 🔳 🚺	01 🛌 🗈	0 <	><	> 3015
Array Information						and the second se
Array ID 40eah5	5ec-h6h6-4265-8					
Array Name BAT 2	5					
Barcode @5105	9900309137041					
Design Tune Express	sion			1 d	1 A 4	
Probe Array Tupe Test3					神聖の間	
Sample File Name C:\Com	mand Console		1. 1. 1. 1. 1.	1000	200 (D) K	
Fluidics		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1			
Eluidics Date			1 an 1 an 1		1 State 1	
Fluidics Module ID			1. 1. 1.	1 . A		
Fluidics Module Num			1 A A A A A A A A A A A A A A A A A A A			
Eluidics Station ID			2	1.000	1 m 1	
Fluidice Station Num			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		241 41	
Fluidice Status			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			
Operator	~		ST 19 16 17		5 m. 1	
ids Full Image 👫 Active Gri	7 ×				13.00%	
ide 🕂 Full Image 🔛 Active Gri	P d ge Processing •					
ids Full Image R Active Gri	ge Processing •	ayo (Acply) _ Sho	w Errors Only	Filter by: Da	te Scanned 🕞	
ids Full Image R Active Gri Full Image R Acti	d v x ge Processing v flows of last: 10 C	ays Apply _ Sho all Positi Scan Status	w Errors Only Array Name A	Filter by: Da	te Scanned 🔹	¢ CEL Genera
ds Full Image Active Gri ofkflow Review Refresh Show Work Date Scanned 9/3/2011 3:11:14 PM	d Processing V ge Processing V flows of last: 10 C # Barcode W @5106310.	ays (Apply) _ Shor H Positi Scan Status Finished	w Errors Only Array Name A @5106810_	Filter by: Da Array Type HG-U133A	te Scanned Grid Alignment Finished	CEL Genera Finished
dt Full Image Active Gri Controllow Review Refresh Show Work Date Scanned 5/3/2011 3:11:14 PM 5/3/2011 3:45.45 PM	g X d ge Processing • flows of last: 10 E Barcode W @5106310.	ayo (Acply) _ Sho hl Positi. Scan Status Finished	w Errors Only Array Name @\$106810_ @\$106810_	Filter by: Da Array Type HG-U133A HG-U133A	te Scanned - Grid Alignment Finished Finished	CEL Genera Finished Finished
ids Full Image # Active Gri Control of the service we Refresh Show Works Date Scanned 5/3/2011 3:11:14 PM 5/3/2011 3:44 5 PM 5/3/2011 4:04:49 PM	# X #	avs Acpby _ Sho hl Positi. Scan Status Finished Finished Finished	w Errors Only Array Name A @5106810. @5106810. @5106810.	Filter by: Da Array Type HG-U133A HG-U133A HG-U133A	te Scanned • Grid Alignment Finished Finished	CEL Genera Finished Finished
id: Full Image Active Gri Conclow Review Refresh Show Work Date Scanned 55/2011 3.411.4 PM 55/2011 3.414 PM 55/2011 3.414 PM	9 X d	ays Apply Sho H PositiScan Status Finished Finished Finished	w Errors Only Array Name @5106810. @5106810. @5106810. @5106810. @5106810.	Filter by: Da Array Type HG-U133A HG-U133A HG-U133A HG-U133A	te Scanned • Grid Alignment Finished Finished Finished	CEL Genera Finished Finished Finished Finished
ids Full Image Active Gri Control of the series Refresh Show Work Date Scanned 5/2/2011 34:45 PM 5/2/2011 4:04 45 PM 5/2/2011 4:04 45 PM 5/2/2011 4:04 45 PM 5/2/2011 4:04 45 PM	# X # X d	ays Apply Sho all PositiScan Status Finished Finished Finished Finished Finished	w Errors Only Array Name A @5106810. @5106810. @5106810. @5106810. @5106810.	Filter by: Da Array Type HG-U133A HG-U133A HG-U133A HG-U133A HG-U133A	te Scanned Grid Alignment Finished Finished Finished Finished Finished	¢ CEL Gener Finished Finished Finished Finished
ids Full Image Active Gri Active Gri Active Gri Active Gri Active Gri Full Image Active Active Gri Full Image Active	# x	ays Apply Sho H PositiScan Status Finished Finished Finished Finished Finished	w Errors Only Array Name / @5106810. @5106810. @5106810. @5106810. @5106810. @5106810. @5106810. @5106810.	Filter by: Da Array Type HG-U133A HG-U133A HG-U133A HG-U133A HG-U133A HG-U133A	te Scanned Grid Alignment Finished Fin	CEL Genera Finished Finished Finished
ids Full Image Active Gri Full Image III Activ		ayo Acpby Sho al Positi Scan Status Finished Finished Finished Finished Finished Finished	w Errors Only Array Name A @5106810. @5106810. @5106810. @5106810. @5106810. @5106810. @5106810. @5106810. @5106810.	Filter by: Da Array Type HG-U133A HG-U133A HG-U133A HG-U133A HG-U133A HG-U133A HG-U133A HG-U133A	te Scanned • Grid Alignment Finished Finished Finished Finished Finished Finished Finished Finished Finished Finished	P CEL General Finished Finished Finished Finished
ids Full Image Active Gri Control Image Active Act	9 X d	ays Apply Sho all PositiScan Status Finished Finished Finished Finished Finished Finished Finished	w Errors Only Array Name A @5106810. @5106810. @5106810. @5106810. @5106810. @5106810. @5106810. @510810. @511320. BAT_25	Filter by: Da Array Type HG-U133A HG-U133A HG-U133A HG-U133A HG-U133A TrueTag_5. Teet3	te Scanned Grid Alignment Finished Fin	CEL Generation Finished Finished Finished Finished Finished Finished

For information on aligning a misaligned grid, see "Checking the grid alignment" on page 310.

🥏 Refresh

Updating the list

Click the Refresh button

in the Toolbar.

Sorting the list for a particular parameter value

Click in the column header for that parameter.

Selecting columns for display

1. Right-click in any column header.

A menu of the column headers appears (Figure 318).

Figure 318 Column Header menu		
Tigure 516 Column neader mend		
Workflow Review		д X
C Refresh Show Workflows of last: 20 Days Apply Show Errors Only Filter by: Date	te Scanned Number of Re	ecord(s): 8
Date Scanned Barcode Well Positi. Scan Status 5/3/2011 311:14 PM @51068100247530010804300015385008 Finished Finished 5/3/2011 314:45 PM @51068100247530010804300015385008 Finished Finished 5/3/2011 34:45 PM @51068100247530010804300015385008 Finished Finished 5/5/2011 1:55:44 PM @51068100247530010804300015385009 Finished Finished 5/5/2011 1:57:24 PM @51068100247530010804300015385009 Finished Finished 5/5/2011 1:4:12 PM @51059001513456712302 Finished Finished 5/5/2011 4:50:11 PM @51059900309137041705400091668901 Finished	* Date Scanned , Type [Grid Alignme * Barcode U133A Finished * Well Position U133A Finished * Scan Status U133A Finished * Scan Status U133A Finished * Array Name U133A Finished * Array Type U133A Finished * Grid Alignment Tag_SK_B Error * CEL Generation S Finished * Date Reviewed Finished Error Hislesage * CEL File Name CEL File Name Last Updated	nt CEL Generation Finished Finished Finished Finished Finished Finished Finished
Ready		.;

2. Select or deselect the desired parameters to conceal and display them.

Changing the filter settings

The window enables you to filter the workflows to display only the workflows of interest.

You can filter the displayed workflows by:

- Date since workflow ran
- Error Status
- Any of the values in the columns.

It also indicates the number of displayed records in the Workflow Review window.

Filtering by Date since workflow ran

1. Enter a value for the number of days for which you want to display records and click Apply (Figure 319).

Figure 319	Filter by Date controls				
Show Work	flows of last: 10 Days Apply				

Displaying errors only

1. Select the Show Errors Only check box (Figure 320)



Filtering by other parameters displayed in the Review window

1. Select the parameter type from the Filter by drop-down list (Figure 321).

2. Enter a value in the Filter by text box.

Note: The Filter by function will filter on parameters that are not being displayed in the Review Window. In addition, Only the workflows with parameters matching the entered value will be displayed.

Changing the other settings of the workflow review window

Changing settings for the Review window

- 1. From the **View** menu, select **Options...**
 - The Options dialog box opens (Figure 322).

Figure 322 Options dialog box
JPEG Creation Compression Ratio (%): 75
Sampling Ratio (%):
Workflow Review Window
Refresh every: 5 (Seconds)
Grid Lines
Grid line color:
Manual Grid Adjustment Apply adjusted coordinates to all channels and exposures
Saving Image display options
Save v
QK Default Cancel

- 2. Select or deselect the following feature:
 - Enable Review Window on startup: turns the Review window on whenever the GCC Viewer is opened.

Note: This change will not take effect until you have stopped and restarted the GCC Viewer.

- 3. Change the value for the Refresh interval to control the frequency of the Review Window updates.
- 4. Click **OK** to close the dialog box and enable the changes.
Opening image files

You can display DAT, CEL, and JPG image files in the GCC Viewer. The Viewer has different functions when viewing different types of files (see "File display differences" on page 276).

You have several options for opening files in the Viewer:

- "Using the search and open dialog box", below
- "Using the open dialog box" on page 296
- "Displaying multiple files" on page 297

Using the search and open dialog box

The Search and Open dialog box enables you to search through the files on the GCC system to find the ones of interest.

The Search and Open dialog box enables you to filter the displayed Sample files by:

- Projects
- File Type
- File Creation Date
- Probe Array Type
- Array Name
- Attribute Value
- Click the Search and Open button in the Viewer tool bar; or From the File menu, select Search and Open....

From the file mend, select **Search and Open...**

The GCC File Open dialog box opens (Figure 323).

Figure 323 File C	pen dialog box	
List of Projects	All projects and data roots Name Grid Array Name Folder Build37EU133a @\$1059900309137041705400091668927.DAT Auto @\$5105990030 C1(Cor Default @\$51059900309137041705400091668927.JAT Auto @\$5105990030 C1(Cor Flat @\$5105900309137041705400091668927.JAT Auto @\$5105990030 C1(Cor GCS1.3 @\$52001900408601102105400477603800.DAT Not @\$52026700458007120505400609420034.DAT Not @\$52026700458007120505400609420034.DAT Not @\$52026700458007.C1(Cor Plus2 @\$52026700458007120505400609420034.DAT Not a @\$52026700458007.C1(Cor %\$52026700458 C1(Cor test two_array_type_JFG-U133A_DAT Auto two_array_typ C1(Cor two_array_type_JFG-U133A_DAT Auto two_array_typ C1(Cor	List of available files
File types Filters controls	two_array_types_Hc-0133A_4.0A1 Auto two_array_typ C:(corvertage) Image: Constraint of the second se	Filter Details
	Arroy Selected Search Files By (Use * for wildcard suffix) Array Name Attribute Value Attribute Open Selected 48 File(s) ()	Buttons

The dialog box displays a list of the files that meet the criteria in the upper right corner (Figure 324). You select the files to display from this list.

Figure 324 Unfiltered file list				
Name	Grid Status	Array Name	Folder Path	^
@51059900309137041705400091668927.DAT	Auto aligned	@51059900309137041705400091668927	C:\Command_Console\Data\Alzheimer Files	
@51059900309137041705400091668927_2.DAT	Auto aligned	@51059900309137041705400091668927	C:\Command_Console\Data\Alzheimer Files	
@51059900309137041705400091668927_3.DAT	Auto aligned	@51059900309137041705400091668927	C:\Command_Console\Data\Alzheimer Files	
@52001900408601102105400477603800.DAT	Not Aligned	@52001900408601102105400477603800	C:\Command_Console\Data\Alzheimer Files	
@52001900408601102105400477603800_2.DAT	Not Aligned	@52001900408601102105400477603800	C:\Command_Console\Data\Alzheimer Files	
@52026700458307120505400609420034.DAT	Not aligned	@52026700458307120505400609420034	C:\Command_Console\Data\Alzheimer Files	
@52026700458307120505400609420034_2.DAT	Not aligned	@52026700458307120505400609420034	C:\Command_Console\Data\Alzheimer Files	
@52026700458307120505400609420034_4.DAT	Not aligned	@52026700458307120505400609420034	C:\Command_Console\Data\Alzheimer Files	
two_array_types_HG-U133A.DAT	Auto aligned	two_array_types_HG-U133A	C:\Command_Console\Data\Cancer Files	
two_array_types_HG-U133A_2.DAT	Auto aligned	two_array_types_HG-U133A_2	C:\Command_Console\Data\Cancer Files	
two_array_types_HG-U133A_3.DAT	Auto aligned	two_array_types_HG-U133A_2	C:\Command_Console\Data\Cancer Files	
two_array_types_HG-U133A_4.DAT	Auto aligned	two_array_types_HG-U133A	C:\Command_Console\Data\Cancer Files	_
@51068100251923030604300127464485 DAT	Auto aligned	@51068100251923030604300127464485	C'iCommand, ConsoleiDataiDefault	>

The upper left corner displays a list of the projects in GCC. The lower left corner displays a set of additional filters you can apply to the file list.

The Filter Details in the lower right corner displays information about the filter criteria that have been applied to the list.

The buttons (Figure 325) allow you to:

Figure 325 Buttons	
Apply Filters	Clear Filters
File Attributes	Open Selected

- Apply Filters Apply selected Quick Filter and Attribute Value Filter criteria
- Clear Filters Clear all applied filters
- **File Attributes** Select attributes to be displayed in File list.
- Open Selected Open selected files in File list
 - 2. Select the project(s) with files you want to list in the Projects list (Figure 326).

Figu	ure 326 Displaying Project List
Figu	Projects Build37EU133a GCO5 1.3 New_Project New_Project3 Plus2 Subfolder Project

- Select File Types from the drop-down list. You can choose from:
 - DAT
 - CEL

Changes made in the Projects and Files filters are reflected instantly in the Filter Details part of the dialog box.

Changes to the Quick Filters and Attribute Value Filters have to be applied by clicking the **Apply Filters** button after selecting.

The Quick Filters (Figure 327) enable you to filter by:

- Date of file creation
- Probe Array Types
- Array Name
- Attribute Value

Quick Filters	Attribute Value Filters	
-File Creation	Date	
From	Thursday , June 28, 2007	~
🔲 То	Thursday , June 28, 2007	~
Probe Array	Types ays Selected By (Lise * for wildcard suffix)	•
Array Name		

- 4. Select a date or range of dates for file creation:
 - a. Select the **From** check box.
 - b. Click the arrow at the date (displays the current date).

A calendar for the current month appears (Figure 328).

Figure 328 From Calendar								
Quick Filters Attri	bute	Value	Filte	ers				
File Creation Dat	e —							
From	Tue	esday	5	Apr	il :	24, 2	007	•
П То	•	I	Ар	ril, 21	007		Þ	7
Probe Array Typ	Sun	Mon	Tue	Wed	Thu	Fri	Sat	
All Probe Arrays	1	20	3	4	5	6	7	•
	8	9	10	11	12	13	14	
Array Name	15	16 23	24	18 25	19 26	20	21 28	
Attribute I	29	30	1	2	3	4	5	
Value		Too	lay:	4/24	/20	07		

c. Select a date for the start of the range. You can move from month to month by clicking the < and > buttons.

If you only select one date, the filter will display only the files created on that date.

To select a range of dates:

- d. Select the **To** check box.
- e. Select a date for the end of the range.
- 5. Select Probe Array Types:
 - a. Click on the down arrow in the Selected Probe Array Types list.

A list of the available probe array types is displayed (Figure 329).

In some cases there may be multiple array models under the same header. in these cases you can click the + button to display the additional probe arrays.

Figure 329 Displaying array types
Figure 329 Displaying array types Probe Array Types Image: Constraint of the stress of th

- b. Select the check boxes next to the probe array types you want displayed in the filtered list.
- 6. Enter text strings for Array Name and Attribute Value (Figure 330).

Figure 33	D Selecting an attribute
-Search Files By (U	se * for wildcard suffix)
Array Name 🛛	k
Attribute M Value	

	You can use the	"*" symbol as	a wildcard in the	Array Name	and Attribute.
--	-----------------	---------------	-------------------	------------	----------------

The Attribute Value filters (Figure 331) enable you to enter values for specific sample attributes.

Figure 331 Attribute Value Filters					
Quick Filters Attribute Valu	ue Filters				
Select Template	~				
Name	Value 🔼				
Sample Name					
Sample Type					
Sample Project					
Sample User	~				
<					
🕝 Enter attribute value (Use	* for wildcard suffix)				
Equal to:	✓				

- 7. To enter values for specific attributes:
 - a. Click the Attribute Value Filters tab (Figure 331).
 - b. Select a template with the attribute you want to search on from the Select Template list (Figure 332).

Figure 332 Select Template						
Quick Filters Attr	ibute Value Filters					
Select Template	Default					
Name	DEC Exp Template					
Gender	Derauk					
Sample Name	•					
Height						
Weight						
<						
Enter attribute	value (Use * for wildcard suffix)					

The list displays only the templates with attributes that are being used in the data. |User| attributes are the attributes created specifically for a particular Sample (ARR) file and are not included in any template list.

The attributes in that template appear in the Name list (Figure 333).

Figure 333 entering va	Selecting lue	g attribute and	
Quick Filters Attrib	oute Value Filters		
Select Template	Default		~
Name		Value	
Gender		Equal to: M	
Sample Name			
Height			
Weight			
<			>
Enter attribute va	alue (Use * for wild	lcard suffix)	

c. Select the attribute and enter a value for it in the Attribute box.

Figure 334	Selecting Limits	
Quick Filters Attri	bute Value Filters	
Select Template	Default	
Name	Value	
Gender	Equal to: M	
Sample Name		
Height	Less than: 20	
Weight		
<		
Enter value(s) fo	r the attribute selected	
Less than:	✔ 20	
Equal to:		
48 Less than:		
Greater than:	11 to:	
Greater than or e Between:	qual to:	

You can perform special searches by using the "*" and "," symbols.

"*" Serves as a wild card function. Using searchstring* will return all arrays that contain an attribute that starts with the search string. Using

 $\mbox{*searchstring}$ will return all arrays that contain an attribute that ends with the search string.

If you select a numerical attribute, you can select from the following limits:

- Equal to
- Less than
- Less than or equal to
- Greater than
- Between (use comma-separated values to set the ends of the range).

Figure 335 Filter details with Status notice
Filter Details
Please use scrollbar to view filters.
Date
No Filters
Array Name
Status Filters Changed: Please press the Apply button.
Apply Filters Clear Filters File Attributes Open Selected

Whenever you change a setting in these filter boxes, you need to apply the changes. A notice appears to that effect in the Filter Details area (Figure 335).

- 8. Click **Apply Filters** after making changes.
- 9. The changes are displayed in the Filter Details section (Figure 336).

Figure 336Filter Details with attributesdisplayed	
Filter Details	
Please use scrollbar to view filters.	^
Attribute Value Default:Gender Equal to: M Default:Weight Greater than or equal to: 20 Project Status Filters applied	

The filtered file list is displayed in the File List (Figure 337).

Figure 337 Filtered file list			
Name	Grid Status	Array Name	Folder Path
two_array_types_HG-U133A.DAT two_array_types_HG-U133A_2.DAT two_array_types_HG-U133A_3.DAT two_array_types_HG-U133A_4.DAT new_Sample_HG-U133A_2.DAT April_16_01.DAT April_16_2.DAT April_16_3.DAT April_16_4.DAT	Auto aligned Auto aligned Auto aligned Auto aligned Auto aligned Auto aligned Auto aligned Auto aligned Auto aligned	two_array_types_HG-U133A two_array_types_HG-U133A_2 two_array_types_HG-U133A_2 two_array_types_HG-U133A_2 two_array_types_HG-U133A_2 April_16_01 April_16_01 April_16_01 April_16_01	C:\Command_Console\Data\Cancer Files C:\Command_Console\Data\Cancer Files C:\Command_Console\Data\Cancer Files C:\Command_Console\Data\Cancer Files C:\Command_Console\Data\Cancer Files C:\Command_Console\Data\Subfolder Project C:\Command_Console\Data\Subfolder Project C:\Command_Console\Data\Subfolder Project C:\Command_Console\Data\Subfolder Project

10. Select the file(s) you want to open from the File list and click the Open Selected button.

The selected file is displayed in the Viewer.

Displaying different file attributes in the File list

1. Click the File Attributes button.

The Choose Column Details dialog box appears (Figure 338).

Figure 338 Choose Column Details dialog box		
Calculus and the second to finder (educ		
files in list view.		
Details:		
Grid Status		
Probe Array		
Design Type		
Scan Date		
Serial#		
Filter		
Station#		
Date Created		
Date Modified		
✓ Folder Path		
OK Cancel		

The dialog box displays a lit of the different characteristics that can be selected for display, with a check box next to each characteristic.

- 2. Select the check box for the characteristics you want to display.
- 3. Click **OK**.

The selected characteristics are displayed in the File list.

Using the open dialog box

The Open dialog box displays a list of all the available image files in the system.

Opening a file using the Open dialog box

 From the File menu, select **Open File**; or Click the **Open File** button in the GCC Viewer tool bar. The Open dialog box opens (Figure 339).

Figure	339 Open dialog box	
Look jrc My Recent Documents Desktop My Documents	Data C C C C C C C C C C C C C C C C C C	
My Network Places	File game: Files of type: DAT files (".dat) Cancel	

- 5. If necessary, use the dialog box tool bar to navigate to the directory with the file.
- 6. Select the file you want to view.
- 7. Click Open.
 - The selected image file is displayed in the GCC Viewer.

You can open more than one file in the GCC Viewer (Figure 340).



Displaying a particular image when you have more than one open

1. Click the tab at the top of the Image Window.

Displaying multiple files

Use the < and > scroll buttons in the Image title bar to scroll through the tabs if necessary (Figure 341).



Different icons are used for DAT and CEL files.

Displaying the full path to a displayed file

- 1. Place your cursor on the file's title bar tab.
 - The full path is displayed below the title bar (Figure 342).

Figure 342 Displaying the path to a file	
Qctober_11_02.DAT HG-U133BC_3.CEL	$\triangleleft \triangleright \mathbf{x}$
C:\Command_Console\Data\October_11_02.DAT	Ŧ

Changing the display of the image

This section explains how to use the Image tool bar controls (Figure 343) for:

- "Examining different parts of the image" on page 300
- "Adjusting the colors and contrast" on page 301
- "Changing the grid and intensity display" on page 302

Figure 343 Image window tool bar for DAT and CEL file	
DAT File tool bar	
Autoscale	
550011_Test_(HT_HG-U133B)_A09	× 4 Þ
	0 🛛 🗱 🧱 🗖 Exp - 100ms
Zoom Color/Contrast Copy Contrast/Brightness	Grid and Exposure Intensity Display
CEL File tool bar	
April_16_01_2.DAT X April_16_01_2.CEL	× 4 Þ
IZ 🔍 🔍 🔲 🧿 🐠 🖻 🛛 📢 🛛 🗡 🚺 👔	Files 👻
	DAT File
	JPG File
	Select file types

Part of the tool bar may be hidden if the GCC Viewer is too small.

Displaying the hidden controls

1. Click on the **Hidden Tool Bar** button = at the right of the toolbar (Figure 344).

Figure 344 Displaying hidden controls	
April_16_01_2.DAT April_16_01_2.CEL April_16_4 + ×	Click here to display hidden controls

The hidden controls are displayed below the tool bar (Figure 344).

Examining different parts of the image

These functions work on DAT, CEL, and JPG files.

The Zoom controls are at the left end of the tool bar.

Figure 345 Zoom controls		
April_16_01_2.DAT April_16_01_2.CEL	∢ ∢	×
i 🗖 🔍 🔍 🔳 🗿 💵 🛌 🗈 🔹 🔍	>	Ŧ
Select In Out Reset		
Zoom buttons		

Zooming in on a selected area of the image

- 1. Click on the **Zoom Select** button
- 2. Click and drag around the area you want to examine in more detail (Figure 346).



- 3. Release the mouse button.
- 4. The selected area is displayed in the GCC Viewer (Figure 346).



Zooming in or out on the whole image

5. Click on the Zoom In button 💽 or the Zoom Out button 🔍

Viewing a different area in magnified zoom

1. Click and drag the image to view the area of interest.

Zooming out

1. Click the **Zoom Reset** button 🤐.

Note: You can also use the Grid box controls to select a particular corner or subgrid for examination (see "Checking the grid alignment" on page 310).

These functions work on DAT, CEL, and JPG files.

Adjusting the colors and contrast



Switching between Gray Scale or Pseudo Color display

1. Click the Gray Scale 🔳 or Pseudo Color 🧿 buttons.

Adjusting the contrast range for the image

1. Click the **Set Contrast** button **I**.

The Set Contrast dialog box opens (Figure 349).

Figure 349 S dialog box	Set contrast	
Intensity scale must	be 0 to 65535	
Minimum Contrast:	0	
Maximum Contrast:	1000	
OK Default Cancel		

- 2. Set the minimum and maximum contrast range.
- 3. Click OK to use the settings; or

Click **Default** to return to the default settings; or

Click **Cancel** to close the dialog box without changing the settings.

You can also use the slide bars in the tool bar (Figure 348) to set the contrast without opening the Set Contrast dialog box.

Using the Autoscale Function

The autoscale function takes the image area you are currently viewing and calculates the intensity to find a better minimum and maximum contrast.

1. Click the **Autoscale** button **a**.

The contrast and brightness are automatically adjusted.

These functions only work when DAT files are displayed (Figure 350).

Changing the grid and intensity display

Figure 350 Image window tool bar, grid and intensity controls (for DAT files only)			
550011_1est_[H1_HG-0133B]_A09			
IZ & Q Q II 🙆) OI 🔺 🗈 🛛 🔍	> 1000 🗱 🧱 🔲 Exp - 100ms		
Autoscale	Cell Grid		
	Intensity		
	Cell		
	Centers		

Displaying cell intensity data

If you have a DAT file open with the associated cell intensity data (CEL) file available, you can view the intensity data in the DAT file Image window.

Display or hide the cell intensity data

Click the Cell Intensity button

The cell intensity data for the array is displayed.

Note: When displaying cell intensity data for certain types of probe arrays, control feature cells that failed the cell summary analysis may be masked. See "Viewing failed control features" on page 277.

Displaying different exposures (GeneTitan expression array plate DAT files only)

Each GeneTitan array is scanned twice, with different exposure times. The image data from both exposures are in the GeneTitan DAT file. You can switch between the different exposures for checking the gridding, etc., by using the Exposure button.

The Exposure button displays the currently displayed exposure time.

Switching between views of the different exposures

1. Click the **Exposure** button.

Figure 351 Exposure button	
NA18524_HTFalconScreen02_20090402_CHBJPT_T02_A02_v1.DAT A05.DAT	4 Þ 🗙
: II 🔍 🔍 🔍 📗 🙆 👀 🛌 📭 🛛 🔇 🔊 🔨 🔊 1000 🧱 🧱 🔲 100ms -	

The other DAT Exposure is displayed.

Displaying different wavelengths (Axiom array plate DAT files only)

Each genotyping array is scanned twice, at different wavelengths. The image data from both exposures are in the genotyping DAT file. You can switch between the different exposures for checking the gridding, etc., by using the Wavelength button.

The Exposure button displays the currently displayed exposure time.

Switching between views of the different exposures

1. Click the Color button.

Figure 352 Wavelength button	
NA18524 HTFalconScreen02 20090402 CHBJPT T02 A02 v1.DAT	4 Þ ×
GC-500	

The other genotyping DAT Exposure is displayed.

Displaying cell centers

The center of each cell on the array can be displayed for certain array types. The centers are visible only when viewing DAT files for probe arrays with sub-grids at a

sufficiently zoomed-in level. The cell center display can be used in evaluating gridding problems.

• Click the **Cell Centers** button .

The cell centers are displayed. (Figure 353)



Displaying the grid corners

The grid can be displayed to evaluate gridding problems and perform manual gridding.

1. Click the Grid Corners button

The outline of the grid is displayed on the image.



The grid cells are not displayed until you have magnified the DAT file so that they are visible. (Figure 355)



See "Checking the grid alignment" on page 310 of this manual for more information about manual gridding.

Changing settings for the grid display

1. From the View menu, select Options...

The Options dialog box opens (Figure 356).

Figure 356	Options dialog box	•
JPEG Creation		
Compression Ratio	(%): [75	+
Sampling Ratio (%):	40	-
Workflow Review V	lindow	
Enable Workflo	w Review Window on startup.	
Refre	esh every: 5 🔶 (Seconds)
Grid Lines		
Grid line color:		~
Manual Grid Adjustr	nent	
Apply adjusted	coordinates to all channels and exp	osures
Saving Image displa	y options	
Save	~	
<u>0</u> K	Default Cancel	

- 2. Select a new color for the grids from the Grid line color drop-down box.
- 3. Click **OK** to close the dialog box and enable the changes.

Saving image display options

You can change the save options for the image display settings. These allow you to apply the same contrast and other settings to different image files.

Changing the Save Options for the image display options

1. From the View menu, select Options...

The Options dialog box opens. (Figure 356)

Figure 357 Option	ns dialog box.
Options	×
JPEG Creation	
Compression Ratio (%):	75
Sampling Ratio (%):	40
Workflow Review Window	
Enable Workflow Review	Window on startup.
Refresh every:	5 (Seconds)
Grid Lines	
Grid line color:	~
Manual Grid Adjustment	
Apply adjusted coordinates	s to all channels and exposures
Saving Image display options	
Save	~
<u>Q</u> K <u>D</u> e	fault <u>C</u> ancel

- 2. Select an option from the Saving Image Display options drop-down box:
 - Do Not Save
 - Save: Save settings from one program session to the next.
 - During the program session: Save settings only until the Viewer is shut down.
- 3. Click **OK** to close the dialog box and enable the changes.

Learning about the image file

The Properties box displays information about the image file displayed in the window. The information can be displayed in alphabetical order, or ordered by different categories, depending upon the type of file displayed:

For a DAT file:

- Array Information
- Fluidics
- Grid Alignment
- Image
- Scanner

For a CEL file:

- Array Information
- Cel
- CEL Summary Report (only for files with CEL Summary Reports)
 - You can click on the Report row first, and then click on the button that appears to open a text display of the CEL Summary report (Figure 358).

	Figure 358 Cel Sur	mmary Report Section	
E	Cel Summary Rep	ort	
	Bright features	0	
	Dim features	5	
	Non-synthesized fea	3	
	Report	Report Type:ICell S 🛄 -	 Click to open the Cell Summary Report
	1 Chataline		

See Appendix C, "Cell summary report" on page 353 for more information.

- Fluidics
- Scanner

F	igure 359	Properties box	
Pro	operties	₽ ×	
	2 ↓ 🖻		Properties tool bar
٦Ü	Array Information]	
	Array ID	19979bea-d368-4769-8	
	Array Name	HuEx 1	
	Barcode	@52026700458307120	
	Design Type	Universal	
	Probe Array Type	HuEx-1_0-st-ta1	
	Sample File Name	C:\Command_Console\	
	Fluidics		
	Fluidics Date	2005-02-24T12:37:00.0	
	Fluidics Module ID	0	
	Fluidics Module Nurr	0 ~	
	Fluidics Station ID	0	
	Fluidics Station Num	0	
	Fluidics Status		
	Operator	dmcint	
	Protocol Name	NA	
	Grid Alignment		
	Grid Algorithm Versic		
	Grid Corners	(547, 454), (18814, 505 —	
	Grid Status	Auto aligned	
Ŧ	Sub Grid Corners	Grid[] Array	
Ξ	Image		
	Created By	echuh	
	File Version	1	

Expand or collapse a component

1. Click on the +/- button to the left of the component.

Sorting the data in a different way

1. Click the **Category Sort** 📰 or the **Alphabetical Sort 1** button.

Grid information

The Grid information category displays information about the main grid and sub-grids:

- Global Grid: Displays the pixel coordinates for the corners of the main grid.
- sub-grids (when available): Displays the pixel coordinates for the corners of each sub-grid. (Figure 360)

	Figure 360 displayed	sub-grids	
			_
	! 2 ↓		
	Probe Array Type	HuEx-1_0-st-ta1	^
	Sample File Name	C:\Command_Console\	
	Fluidics		
	Fluidics Date	2005-02-24T12:37:00.0	
	Fluidics Module ID	0	
	Fluidics Module Nurr	0	
	Fluidics Station ID	0	
	Fluidics Station Num	0	
	Fluidics Status		
	Operator	dmoint	
	Protocol Name	NA	
	Grid Alignment		
	Grid Algorithm Versic		
	Grid Corners	(547, 454), (18814, 505	
	Grid Status	Auto aligned	
	Sub Grid Corners	Grid[] Array	
	[0]	(545, 453), (1971, 458),	
	[1]	(1944, 458), (3377, 461	
	[2]	(3350, 461), (4784, 465	
	[3]	(4757, 465), (6189, 469	
	[4]	(6162, 469), (7595, 473	
	[5]	(7568, 473), (9001, 477	
	[6]	(8974, 477), (10407, 48	
	[7]	(10380, 481), (11813, 4	
	[8]	(11786, 485), (13219, 4	
	[9]	(13192, 489), (14625, 4	
	[10]	(14598, 493), (16032, 4	
	[11]	(10000 407) (17400 E	-

Checking the grid alignment

This chapter describes the use of the GCC Viewer for aligning failed grids:

- "Aligning the main grid" on page 310
- "Aligning sub-grids" on page 314
- "Aligning sub-grids on GeneTitan arrays" on page 320
- "Regenerating intensity values" on page 322

For general information about grid alignment, see "Array and grid types" on page 268.

Aligning the main grid

If the array has sub-grids, the main grid has to be aligned before aligning the subgrids.

If the main grid is misaligned, you will see a notice in the Review list (Figure 361).

Figure 361 No	tice of failed g	rid alignme	nt			
Workflow Review						т х
Show Work	flows of last: 20 Da	ays Apply	Show Errors Only	Filter by: Date Scan	ned 👻	Number of Record(s): 12
Date Scanned	Array Type	Grid Alignment	CEL Generation	Date Reviewed	Error Message	DAT File Name
🥪 5/3/2011 4:04:49 PM	HG-U133A	Finished	Finished			@51068100247530010804300015385008
🧔 5/5/2011 1:55:45 PM	HG-U133A	Finished	Finished	5/9/2011 11:09:48		@51068100247530010804300015385009.[
8 5/5/2011 4:41:22 PM	TrueTag_5K_B	Error		5/15/2011 10:51:28	GridAlignment.exe: Failed	@51133200123456101006123456712302_
8 5/15/2011 11:14:24 AM	TrueTag_5K_B	Error			GridAlignment.exe: Failed	@51133200123456101006123456712302
8 5/15/2011 11:17:43 AM	TrueTag_5K_B	Error			GridAlignment.exe: Failed	@51133200123456101006123456712302
🧕 5/15/2011 11:19:10 AM	Test3	Finished	Finished			BAT_25_3.DAT
٢		ш				

Viewing the main grid

1. Click the **Full Image** button **Full Image** in the Grids tool bar (Figure 362).

The main grid is displayed for single-grid and multi-grid files.

You have two options for fixing an alignment problem:

- You can run the gridding algorithm again.
- You can align the grid manually.

Note: Realigning the grids will update DAT headers and break the parent-child relationship between DAT files and existing CEL files until the CEL files are regenerated.

Running the gridding algorithm

In some cases you can realign the grid by running the alignment algorithm again.

Figure 362 Grid box tool	bar
Grids	д х
🗧 🔚 Full Image 🔛 Active	Grid 🛛 💽 🧱 🧱
	mage Processing 👻
	Realign All Grids
	Realign Sub Grids Only
	Regenerate CEL Intensity

Running the alignment algorithm on an array that uses a single grid

2. In the Grids tool bar, click on the **Image Processing** button Image Processing and select **Realign All Grids** from the shortcut menu. (Figure 362)

A notice informs you that a new cell intensity data file (CEL) will be generated.

Figure 363 Notice of regridding
Re-aligning the grid will break the link to the existing CEL data files. Grid alignment will be automatically followed by cell generation and cell summary report. Do you want to continue? Yes No

3. Click **Yes** to proceed with the alignment.

Progress bars display the progress of the alignment and cell generation.

Figure 364	Progress bar
Grid Alignment	

When the process is finished, a notice appears. (Figure 365)

Figure 365 Notice
Algorithm was executed successfully.

New gridding information and a new CEL file are generated.

Aligning the grid manually

If the algorithm alignment fails, an error message appears. (Figure 366)

Figure 366	Notice of main grid misalignment
Failed to execute the G	and Alignment algorithm.
The error is: Failed to f	Ind the grid corner pattern. Please use the Command Console Viewer to verify that the corner locations do not have any smudges or crossover patterns
that may cause the alg	orithm to fail.

If you see the error message, you can manually adjust the main grid by using the following procedure:

1. Click on the failed DAT file in the Review window.

The main grid is displayed in the Image window. (Figure 367)



2. Align the grid at each corner of the image:



 a. Click a Corner button in the Grid box toolbar (Figure 368) to choose a corner. The selected corner is displayed in the Image window. (Figure 369) The software displays a box around each feature of the corner grid.



b. Place the mouse arrow over the grid perimeter (the arrow becomes a double arrow, ↓

The diagonal orientation of the double arrow along the perimeter of a corner probe cell indicates horizontal and vertical adjustments can be made simultaneously using the click-and-drag method or by using the keyboard arrow keys.

c. Use the click-and-drag method or the keyboard arrow keys to adjust the horizontal or vertical position of the grid so that it is aligned over the corner of the outermost corner checkerboard.

- d. Repeat the above steps for the other corners of the main grid.
- 3. After you align the grid, click the **Save** button $\boxed{\begin{subarray}{c} Save} \end{subarray}$ or select **File** \rightarrow **Save** from the menu bar.

A notice opens, informing you that a new cell intensity data file will be generated automatically. (Figure 370)

Figure 370	Notice
Updating the grid wi	I break the link to the existing CEL data files. CEL file generation will be executed automatically.
Do you want to cont	inue?

4. Click **Yes** to save the DAT file and generate a new CEL file.

The cell intensity data file will be generated automatically.

For arrays with a single grid, you can now proceed to generate the CEL file (see "Regenerating intensity values" on page 322).

For arrays with sub-grids, you can now check the alignment of the sub-grids (see "Regenerating intensity values", below).

Aligning sub-
gridsSometimes one or more sub-grids may require alignment. The failed sub-grids are
marked with an X in the Grids box (Figure 371).

If the sub-grid alignment fails you can:

- Run the sub-grid alignment algorithm.
- Perform a manual alignment on the failed sub-grids.

Note: Realigning the grids will update DAT headers and break the parent-child relationship between DAT files and existing CEL files until the CEL files are regenerated.

Running the sub-grid alignment algorithm

You can run the sub-grid alignment algorithm if some of the sub-grids are misaligned or if you have manually aligned the main grid.

to Decligning the grid

Running the alignment algorithm again on an array that uses sub-grids

1. In the Grids toolbar, click on the Image Processing button Timage Processing • and select Realign All Grids from the shortcut menu. (Figure 372)

Figure 372 Grids tool ba	ar for array with sub-grids
1	
Grids	- 4 ×
🕴 🔄 Full Image 📑 Active	Grid 🛛 🎆 🧱 🔣 🚽 —————————————————————————————————
11 🏥 🖬 🖬 🖬 🖬	mage Processing 👻
	Realign All Grids
	Realign Sub Grids Only
	Regenerate CEL Intensity

A notice informs you that a new cell intensity data file (CEL) will be generated. (Figure 373)

Figure 373	Regridding notice
Re-aligning the grid Do you want to cor	will break the link to the existing CEL data files. Grid alignment will be automatically followed by cell generation and cell summary report. tinue? Yes No

2. Click **Yes** to proceed with the alignment.

Progress bars display the progress of the alignment and cell generation. (Figure 374)

Figure 374	Progress bars
-	
Grid Alignment	

When the process is finished, new gridding information and a new CEL file are generated and will align the main grid and all sub-grids.

Running the sub-grid alignment algorithm only

1. In the Grids toolbar, click on the Image Processing button in Image Processing ▼ and select Realign sub-grids Only from the menu. (Figure 372)

A notice informs you that a new cell intensity data file (CEL) will be generated. (Figure 375)

_	_	-	_	_	
			>		
		r.,	85.		
		1	í₽	1	
		1	2	1	
		6	-		

Figure 375 Cl	EL generation notice
Re-aligning the grid will be Do you want to continue?	reak the link to the existing CEL data files. Grid alignment will be automatically followed by cell generation and cell summary report. Yes No

2. Click **Yes** to proceed with the alignment.

Progress bars display the progress	of the alignment ar	nd cell generation.
(Figure 376)		

Figure 376	Progress bars
Grid Alignment	

When the process is finished, new gridding information and a new CEL file are generated.

Manually aligning the sub-grids

The boundaries of a sub-grid are indicated by the alignment patterns at the four corners of the sub-grid. A small checkerboard may mark the corner of two or more sub-grids, depending upon its position in the main grid. (Figure 377)

Figure 377	sub-grid bord	ders					
eta Dan Dala							
Elle Mew Delh		10.1					
Search & Open	🍯 Open File 🔛 Save	Help					
Properties	д х	📕 Hu	Ex 1.DAT				4 Þ :
8≣ 2↓ 🖻		्र 🖸	Q Q 🔳 🕻) 🚺 🛌 🗎	0 <	><	>
Array Information	n 🔥	- 22	Contraction of the local division of the loc				22
Array ID	19979bea-d368-4769-8	8					3
Array Name	HuEx 1						The second second
Barcode	@52026700458307120						
Design Type	Universal						
Probe Array Type	HuEx-1_0-st-ta1	Sal Cash					
Sample File Name	C:\Command_Console\	4					
3 Fluidics							
Fluidics Date	2005-02-24T12:37:00.0						
Fluidics Module ID	U 🗸	•					
Pride							
	··· ··· · · · · · · · · · · · · · · ·						
Full Image 🖪 A	Active Grid						
P P P P P	🚊 Image Processing 👻						
		4					
							<u> </u>
							4
		<					>
ivel Y = 4583 Divel V	- 8853 Intendity - 14						
1761 A = 4505, FIXELT	- 0055, Intensity - 16						

If the sub-grids are not aligned correctly, the following error message appears after imaging an array or opening a DAT file: (Figure 378)

Figure 378	Notice of sub-grid misalignment(s)
Failed to execute the The error is: Failed to Command Console Vier	Grid Alignment algorithm. update the DAT file. The file may be in use. Please close any application that may have the DAT file open. The grid may have to be aligned through the wer. OK

Navigating from sub-grid to sub-grid

The failed sub-grids are marked with an X in the Grids box. (Figure 379)



Highlighting

- Selected sub-grids are highlighted in blue
- Selected misaligned sub-grids are highlighted in yellow
- Modified sub-grids are highlighted in green.

Note: You can step through sub-grids using the right and left buttons. (Figure 380)



Stepping through all sub-grids

- 1. Toggle the Step button to the all position
- 2. Click the left and right buttons to step through the sub-grids.

Stepping only through the misaligned grids

- 1. Toggle the Step button to the misaligned position.
- 2. Click the left and right buttons to step through the sub-grids.

Manually align a failed sub-grid

- 1. Click **OK** in the sub-grid Alignment Failure dialog box. (Figure 378)
- 2. Click on the sub-grid you want to align in the Grid box.
- 3. A zoomed-in view of the sub-grid appears in the Image window. (Figure 381)



- 4. Align the sub-grid at each corner:
 - a. Click the Go To Corner button for the corner you want to align.
 A zoomed-in view of the corner of the sub-grid appears. (Figure 382)



b. Place the mouse arrow over the grid perimeter (the arrow becomes a double arrow, ↓

The diagonal orientation of the double arrow along the perimeter of a corner probe cell indicates horizontal and vertical adjustments can be made simultaneously using the click-and-drag method or by using the keyboard arrow keys.

c. Use the click-and-drag method or the keyboard arrow keys to adjust the horizontal or vertical position of the sub-grid so that it is aligned over the outside corner of the small checkerboard pattern. (Figure 383)

Figure 383	Dragging the su	b-grid bounda	ary	
<u>File ⊻iew H</u> elp				
🚰 Search & Open	🚰 Open File 🛃 Save 🛛 🕢 He	dp		
Properties	7 X	HuEx 1.DAT*		4 Þ
ê≣ 2 ↓ 🔤	5	ି ଓ ଓ 🔲 🗿 🛛	💽 🛌 🗈 🛛 33 🔇	
Array Information			The second s	
Array ID	19979bea-d368-4769-8	N M 13	ing the second	医马马克氏 医结合的
Array Name	HuEx 1	しょうし いわざい	e fi shinaka	i and in the second second
Barcode	@52026700458307120	Same - Marine (
Design Type	Universal	101 - 104 A.		
Probe Array Type	HuEx-1_0-st-ta1		a fill a state of the second sec	
Sample File Name	C:\Command_Console\	kan kumpungt	State 1 1 1 1 1	the second se
E Fluidics	0005 00 04740 07 00 0			and the second second
Fluidics Date	2005-02-24112:37:00.0			
Fluidics Module ID				
Grids	л x -			
		나는 나는 눈 바람 걸렸다.	이 지 않는 것이 같이 있다.	
	🕂 Image Processing 👻	1771 1774 17. 78	Gente vite de	승규는 이 가슴을 가 봐야?
			والمتعاد والمتعاد والمتعاد	
		는 11.11 는 11.11.45 (P. 16.45)	ante l'ante	and the second secon
				and the second second
				The second s
			10. TO 10.	10 C
		医乳糖 计图合数	en de la constituir de la	
			The second s	and the second
		그는 아이에 가지 않는 것이 없다.	이 아이는 이 방송 가장	100
				1991 - 1952 - 1952 - 1952 - 1952 - 1952 - 1952 - 1952 - 1952 - 1952 - 1952 - 1952 - 1952 - 1952 - 1952 - 1952 -
		hand a state of the	KA KA10548	BY 1978
		المراجعة التعري	오프트 이는 것을 했다.	NG
Pixel X = 16024, Pixel	/ = 502. Intensity = 38			

- d. Repeat steps A through C for the other corners of the sub-grid.
- 5. Continue manually aligning all misaligned sub-grids.
- 6. After you align the grid, click the **Save** button **J** Save or select **File** → **Save** from the menu bar.

The Save Notice appears. (Figure 384)

Figure 384 Save notice
Updating the grid will break the link to the existing CEL data files. CEL file generation will be executed automatically. Do you want to continue?
<u>Y</u> es <u>N</u> o

7. Click Yes to save the file.

The file is saved and CEL file generation is done.

Aligning subgrids on GeneTitan arrays

You use the same controls and steps to align sub-grids for GeneTitan arrays as you do for cartridge arrays, with the following exceptions:

You do not need to perform a main grid alignment

- You may have to check the grid alignment for both exposures (see "Displaying different exposures (GeneTitan expression array plate DAT files only)" on page 303) or both wavelengths (see "Displaying different wavelengths (Axiom array plate DAT files only)" on page 303.
- You can select an option to apply adjusted coordinates to all channels and exposures (see "Changing the manual grid adjustment setting" on page 321



Changing the manual grid adjustment setting

You can apply the coordinate adjustments made to one exposure time or channel to the other exposure time or channel.

Changing settings for the manual grid adjustment

1. From the View menu, select Options...

The Options dialog box opens. (Figure 386)

Figure 386	Options	dialog box.		
1				
JPEG Creation	(5-1	br		
Sampling Ratio (%):	40 •		
Workflow Review	Workflow Review Window			
Enable Workfi Ref	resh every: 5	dow on startup.		
Grid Lines				
Grid line color:		~		
Manual Grid Adjust	Manual Grid Adjustment			
Apply adjusted	Apply adjusted coordinates to all channels and exposures			
Saving Image display options				
Save V				
<u>о</u> к	<u>D</u> efault	t <u>C</u> ancel		

- 2. Select or deselect the Manual Grid Adjustment check box.
- 3. Click **OK** to close the dialog box and enable the changes.

Regenerating intensity values

Cell intensity values are generated automatically after:

- Running any grid alignment algorithm.
- Saving a DAT file after manual gridding.

You can also regenerate the intensity values without performing one of these other steps.

Regenerating the intensity values

- 1. In the Grids toolbar, click the Image Processing button 🛱 Image Processing -
- 2. Select Regenerate CEL Intensity from the list.

A new CEL intensity data file will be generated. It will automatically have an underscore and number appended to the name to distinguish it from a previously generated file.

Exporting images in other formats

You have two options for exporting a copy of the image:

- "Copying images to the computer clipboard"
- "Creating a JPG file" on page 323

Copying images to the computer clipboard

1. Display the image you want to copy in the Image window.

Note: You can zoom in on a specific region of the image if you desire before copying.

- 9
- 2. Click the Copy button in the image window tool bar (Figure 387) or press Ctrl c.

Figure 387 Copy button			
April_16_01_2.DAT April_16_01_	_2.CEL 📄 4 🕨 >	×	
: IZ @ @ Q II @ II 🔺 🗈 👘	0 <)	Ŧ	
Copy button			

The image is now copied to the clipboard.

You can then paste the image into a graphics program such as MS Paint, then save the file as you normally would.

Creating a JPG file

You can create a JPG copy of a DAT file for archive purposes.

Creating a JPG copy of a DAT file

 From the File menu, select Create JPG from DAT.... The Open dialog box opens. (Figure 388)

Open						
$ ightarrow \star \star$ 🎾 > Sea	rch Results in Downloads \Rightarrow			✓ Ö Searc	h Search Results in Dow	
)rganize 🔻						
A Quick accord	Name	Date modified	Туре	Size	Folder	
	55048443408311013	3/29/2018 1:55 PM	DAT File	589,986 KB	Default (C:\Users\	
Desktop 🖈	55048443408311013	3/29/2018 1:49 PM	DAT File	589,986 KB	Default (C:\Users\	
🕂 Downloads 🖈	55048443408311013	3/29/2018 1:48 PM	DAT File	589,986 KB	Default (C:\Users\	
🚆 Documents 🖈	55048443408311013	3/29/2018 1:47 PM	DAT File	589,986 KB	Default (C:\Users\	
📰 Pictures 🛛 🖈	55048443408311013	3/29/2018 1:46 PM	DAT File	589,986 KB	Default (C:\Users\	
Command_C 🖈	55048443408311013	3/29/2018 1:45 PM	DAT File	589,986 KB	Default (C:\Users\	
Logs 🖈	55048443408311013	3/29/2018 1:44 PM	DAT File	589,986 KB	Default (C:\Users\	
deenlaser-1.8	55048443408311013	3/29/2018 1:44 PM	DAT File	589,986 KB	Default (C:\Users\	
Puplog *	55048443408311013	3/29/2018 1:42 PM	DAT File	589,986 KB	Default (C:\Users\	
	55048443408311013	3/29/2018 1:41 PM	DAT File	589,986 KB	Default (C:\Users\	
Default 🛪	55009442002161017	3/20/2018 4:18 PM	DAT File	589,980 KB	sanita (C:\Users\af	
Command C 🖈	55009442002161017	3/20/2018 4:13 PM	DAT File	589,980 KB	sanita (C:\Users\af	
🖵 airwin 🛛 🖈	XHMSUCCD	3/29/2018 2:29 PM	File folder		Tasks (C:\Users\af	
sanita 🖈	Tasks	3/29/2018 2:29 PM	File folder		3-29-2018 12 28 03	
📕 TFCDeepLase 🖈	TipTiltCal	3/29/2018 2:29 PM	File folder		Tasks (C:\Users\af	
backup	SUTSHUT	3/29/2018 2:29 PM	File folder		Tasks (C:\Users\af	
Configuration	STATMGR	3/29/2018 2:29 PM	File folder		Tasks (C:\Users\af	
log	Suhas Exp	3/29/2018 2:29 PM	File folder		S96PROC (C:\User	
	Archives 3	3/29/2018 2:29 PM	File folder		S96PROC (C:\User	
Log 3-26-2018 -	S96PROC	3/29/2018 2:29 PM	File folder		Tasks (C:\Users\af	
🕋 OneDrive 🔍 🗸	Archives	3/29/2018 2:29 PM	File folder		Archives 2 (C:\Use	
File na	me 550494424092110121909	7 (Avien LIKE WCSG	07.047	DAT	Filer (* dat)	

- 2. Select the DAT file you want to copy.
- Click Open.
 The JPG file is created.

Viewing the JPG file

1. Click File \rightarrow Open File.

An Open window appears.

- 2. Navigate to the file's location as you normally would.
- 3. Click to highlight it, then click **Open**.

The selected image file is now displayed in the Viewer.

- 1. Opening the JPG in the Windows Picture and Fax Viewer
- In the Folder View, click the Explore link next to the JPG file.

The selected JPG file is displayed in the Windows Picture and Fax Viewer.

Changing settings for the JPG conversion

1. From the View menu, select Options...

The Options window appears. (Figure 389)

Figure 389 Options window			
Options	×		
JPEG Creation Compression Ratio (%): Sampling Ratio (%): Workflow Review Window	75 🚖 40 文		
Enable Workflow Review Window on startup. Refresh every: 5 (Seconds)			
Grid Lines			
Grid line color:	~ ~		
Manual Grid Adjustment Apply adjusted coordinates to all channels and exposures			
Saving Image display options Save			
<u>Q</u> K <u>D</u> efault	Cancel		

2. Change the values for Compression Ratio and Sampling Ratio.

Increasing either of these values increases the resolution of the JPG image, but also increases the size of the JPG file.

3. Click **OK** to close the dialog box and enable the changes.


Probe array types

Changing probe array types

GCC enables you to change the probe array type for any or all of a group of files.

The Change Probe Array Type function enables you to:

- Change the probe array type for the selected Sample and data files, regrid the associated DAT files, and regenerate the associated CEL files
- Change the probe array type field for selected CEL files

You might want to use this function:

- If you are working with probe arrays that can be used for more than one type of analysis.
- If you have analyzed a set of prototype arrays using a preliminary set of library files, and you now have the correct library file set.

Note: The Change Probe Array Type function cannot be used for GeneTitan Array Plates.

1. Select the files for which you which to change the probe array type.

You can select files to change from:

- The Folder View (see "Selecting files" on page 57).
- The Project View (see "Selecting files" on page 65).
- The Search Results page (see "Selecting files" on page 75).
- Select Change Probe Array Type from the Command to Run drop-down list. The Change Probe Array Type page opens. (Figure 390)

Figure 390 Change Probe Array Type page					
Search Files By: Array Name 💌 (Use * for wildcard) 🔤 <u>Advanced Search</u>					
Change Probe Array Type 🖬					
♥ Nou have several different options. ● Realign the grids of DAT files and regenerate CEL files, overwriting existing files. ■					
○ Change only the probe array type of a selected CEL file. ■					
After you have made your choice, click on the "Next" button in order to select the DAT files and/or CEL files to process.					
Back Next Cancel					

3. Select the option you want to use:



- Realign the grids of DAT files and regenerate CEL files, overwriting existing files.
- This option will:
 - Change the probe array type for the selected Sample and data files
 - Re-grid the associated DAT files
 - Regenerate the associated CEL files and the cell summary report file

IMPORTANT! Realigning the grids will break the parent-child relationships between DAT files and CEL files and between CEL files and CHP files until the CEL files are regenerated (Any CHP files are not automatically regenerated; you must regenerate them manually). Choosing this action will not delete any vital information because you can change the probe array type back to its original value if you change your mind.

• Change only the probe array type of a selected CEL file.

This option will only change the probe array type information in the selected CEL file(s). It does not modify the Sample probe array type information in the Sample file or the DAT file.

This option is for use when using a CEL file that belongs to a multi-use array. These arrays that can be analyzed in multiple ways, as an Expression array or a Genotyping array.

4. Click Next.

The page displays the data files. (Figure 391)

ou have	chosen to realign the grids	of DAT files and regenerat	e CEL files, overwriting existing files.	
	DAT file	CEL file	Probe Array Type	Result
	FlovArryName.DAT	(Missing CEL file)	HG-U133A_2	
~	FlowArryName.DAT	FlowArryName.CEL	HG-U133A	
	FlowArryName.DAT	HG-U133A		
ange th Back	ne probe array type for the	selected files to: E <u>coli_2</u>	M	

5. Select the files to be changed by selecting the check boxes in the left-hand column.

You can use the **Select All** and **Deselect All** buttons to select all or deselect all files.

6. Select the probe array type you want to change the selected files to from the drop-down list. (Figure 392)



Figure 392 File Type list	
Change the probe array type for the selected files to: Back Next	E_coli_2

7. Click Next.

The page displays the progress of the transformations. (Figure 393)

Figure 393 Progress of probe array type changes								
Search Files By: Array Name (Use * for wildcard) Advanced Search								
Chang	e Probe Array Ty	pe						
You have	e chosen to realign th	ne grids of DAT files ar	nd regenerate CEL files, overwrit	ing existing files.				
	DAT file	CEL file	Probe Array Type	Result				
	FlowArryName.DAT	(Missing CEL file)	HG-U133A_2					
2	FlowArryName.DAT	FlowArryName.CEL	HG-U133B	Successfully changed the probe array type.				
Change t	he probe array type	for the selected files t	o: HG-U133B					



Administration functions

The Administration functions provide additional options for organizing and tracking your data:

- "Working with templates"
- "Tracking the workflow" on page 336

Working with templates

Templates are used to organize a set of attributes that you can use to create a new Sample file.

Attributes are properties used to describe a sample and its associated array(s). Attributes include:

- Sample Name
- Gender
- Date
- Array Type
- Array Barcode

When you create a template, you specify:

- the attributes included in the template
- the data type for each attribute:
 - Text: text string
 - Number: Floating point or Integer
 - Date: Calendar data
 - SingleSelect: enables the user to select a single item from a controlled vocabulary list
- whether the attribute is required
- value options for SingleSelect attributes

Templates allow you to organize attributes and collect consistent data for your experiments and samples.

The following templates are included in the GCC install:

- MIAME sample information
- Pedigree template

This section describes the following functions:

- "Creating a template", below
- "Editing a template" on page 331
- "Deleting templates" on page 333
- "Managing default templates" on page 335

Creating a template

From the Templates menu, select New Template.
 The Create Template File page appears. (Figure 394)

Figure 394 Create Template File page	
Search Files By: Array Name V (Use * for wildcard) Advanced Search C Advanced Search ADMINISTRATION HELP)
Create Template File	
A template defines the input fields used in data entry when creating or editing Array Attribute files.	
Euter Template File Name July_Template Next	

2. Enter a name for the template and click **Next**.

The Add Attributes page opens. (Figure 395)

Figure 395 Edit Template	es page			
Search Files By:	Array Name	~	(Use * for wildcard)	Advanced Search
HOME DATA SAMPLES ADMI	NISTRAT	ION HELP)	
Template Name July_Template	2			
Sample Attribute Name	Required	Туре	Control Vocabulary*	Default Value
		Text 💌 Text		
Delete		Number Date		
*To use controlled vocabulary select Single	Select as the	SingleSelect	e value on each line.	
		(Save	



The page displays a list of the attributes for the template.

Adding a field to the list

1. Click Add.

A new row appears in the list, with the following boxes for entering information or links:

Sample Attribute Name	Enter a name for the attribute.	
Required	Click if the attribute is required.	
Туре	 Select from drop-down list: Text: Text string Number: Integer or floating point number Date: Calendar data SingleSelect: Presents a list of items for the user to choose 	I Type Text Text Number Date O SingleSelect

Control	Enter values for the controlled vocabulary, placing multiple values on
Vocabulary	separate lines.

Default Value Enter a default value to be displayed for the field in a new Sample file.

- 2. Enter or select values for the field characteristics.
- 3. Repeat Step 1 and Step 2 for the other attribute fields you want to add.
- 4. After creating the attribute fields, click Save to save the template.

The Results Page displays the name of the created template (Figure 396).



Figure 396 Result page	
Search Files By: Array Name V (Use * for wildcard) Advanced Sear	rch 🤄
HOME DATA SAMPLES ADMINISTRATION HELP	
Result Page 🖬	
The template July_Template was saved successfully.	

Editing a template

You can edit an existing template.

Note: Deleting an attribute from a template or changing data type will cause attribute discrepancies if you have already used the template to create Sample files. For more information, see "Sample attributes conversion" on page 115.

1. From the Templates menu, select Edit.

The Edit Template File page appears. (Figure 397)



Figure 397 Edit Template File	
Search Files By: Array Narre V (Use * for wildcard) Advanced Search HOME DATA SAMPLES ADMINISTRATION HELP	٩
Edit Template File	
A template defines the input fields used in data entry when creating or editing Array Attribute files.	
Select Template File	
Next	

 Select the template you want to edit and click Next. The Add Attributes page opens. (Figure 398)

Figure 398 Add Attribute	s page			
Search Files By: HOME DATA SAMPLES ADMIN	Array Name	ION HELP	(Use * for wildcard)	Advanced Search 🛛 🖗
Template Name July_Template	?			((
Sample Attribute Name	Required	Туре	Control Vocabulary*	Default Value
Gender		SingleSelect 🗸	F	
			171 	
Tissue Type	$\overline{\checkmark}$	Text 🗸		
Delete Add				
*To use controlled vocabulary select Singles	Select as the	Type. Enter on	e value on each line.	
		G	-	
		C	Save	

You can add, edit, or delete fields with the same functions used to create a new template. For more information see "Creating a template" on page 329.

After editing the attribute fields, click Save to save the template.
 The Results Page displays the name of the created template.

Figur	e 399	Results	page					
HOME	DATA	Search I SAMPLES	iles By: ADMI	Array Name	N HELP	(Use * for wildcard)	Advanced Search	٩
Result	Page 😫							
т	The templ	ate July_Tem	plate was	saved success	fully.			

Deleting templates

You can delete a template from the list.

Note: Deleting a template will cause attribute discrepancies if you have already used the template to create Sample files.

1. From the Administration menu, select **Templates** \rightarrow **Delete**.

The Delete Template File page appears. (Figure 400)



Figure 400 Delete Template File page			
Search Files By: Array Name	(Use * for wildcard)	Advanced Search	٩
Delete Template File 🖾 A template defines the input fields used in data entry when creating or editing	Array Attribute files.		
Select Template File to Delete			

- 2. Select the template to be deleted from the drop-down list.
- 3. Click Delete.

The template is deleted. (Figure 401)

Figure 401	Notice of template deletion	
HOME DATA	Search Files By: Array Name V (Use * for wildcard) Advanced Search	٩
Delete Templa A template de You are about t	late File Image: state of the input fields used in data entry when creating or editing Array Attribute files. to delete the Template 'new'. Press Yes to continue or No to cancel Yes	

11

Managing default templates

The default template attributes are displayed when the Detailed Sample Registration function is used and are displayed in the Default view in Folder view.

Changing the default templates

1. From the Administration menu, select $\textbf{Templates} \rightarrow \textbf{Default}.$

The Default Template File page appears. (Figure 402)

Figure 402 Manage Default Templates page	
Search Files By: Anay Name (Use * for HOME DATA SAMPLES ADMINISTRATION HELP	wildcard) 🛛 <u>Advanced Search</u> 🕀
Defaults Image: Constraint of the second	and are displayed in the Default view in plates Default Template Details ult

Click on a template name to see a list of the attributes in that template. (Figure 403)

Figure 403	Template Details		
Default Templa	ıtes		
	Default Template Details		
Default	Sample Name Gender Weight Height		

- 2. Select the template(s) to be defined as default templates from the Available Templates list.
- 3. Click Add.

The template is moved to the Default Templates list.

You can also click the **Remove** button to remove templates in the Default Templates list.



The template attributes will be available in the Detailed Sample Registration page. (Figure 404)

Figure 404	Detailed Samp	le Registration pag	e with default Template attributes
Se	arch Files By: 🛙 🗛 🗛	Name 🗸	(Use * for wildcard) 2 Advanced Search
HOME DATA SAM	ADMINIST	RATION HELP	
Detailed Sample Re	gistration 💷		
Selected Project: 💷	~		
Sample File Name(R	equired):		
Sample Attributes from	n Templates(Optional)		
Default			×
Sample Name (Requi	red): Text		
Gender (Required):	SingleSelect 🔜 💌		
Weight (Required):	Number		
Height (Required):	Int		
	Select Opti	ons	
Select template name fro	m the drop-down list and	click "Select" to use the template for	r this sample. Click "Options" to change which templates to use to for this sample.
Additional Sample Att Click "Add" to add anot	ributes(Optional) her item that will be collect	ted in addition to fields collected fro	m the templates
Name		Value	
Delete	dd		
Name refers to the label	of the data. Value refers to	odata. Example if you wanted to c	allect a comment you might set Name to "Comment" and the Value to "Here is my
comment."	of the data. Value refers t	o data. Example 1 you wanted to e	acet a comment you might set rune to comment and the value to receip ing
Arrays		Derive	array names from sample file name
Barcode		Probe Array Type	Array Name
		×	
Lot Number:	Expiration Date:		
Delete Ad	ld		
Click "Add" to add an am	ray to this sample. Select a	check box next to an array and cl	ck "Delete" to remove an array.
Checking "Derive array n	ames from sample file nam	e" will default the Array Names (fil	e name for DAT, CEL and CHP) to be based on the Sample File Name.
sarcode will automatically	y select the Probe Array 1	ype. Barcode is not required.	Cancel
		Save	Cancer

Tracking the workflow

The Workflow Monitor page enables users to view a list of the arrays in the workflow and see what their status is.

Viewing the Workflow Monitor page

1. Click Administration \rightarrow Workflow.

The Workflow Monitor page opens (Figure 405).



Figure 405 Workf	low Monitor page					
5	Gearch Files By: 💷 🛛 Array Na	me 🔽	(Use *	for wildcard) 🗾 Advar	<u>nced Search</u>	
HOME DATA SAMPLES	ADMINISTRATION HEL	P				
Workflow Monitor 💷						
Use the Workflow Monitor	to view a list of the array	s in the workflow and tr	ack their progress.			
Barcode	Array Name	Probe Array Type	Array/Sample File	Workflow step	Project St	atus
@51133200123456101006123456	712302 @511332001234561010061	23456712302 TrueTag_5K_B.Univer	sal @51133200123456101006123456	712302.ARR Scanning	Default Ru	nning
goli con	Without Without Control of Contro			eesting	Paradis Ind	

The Workflow Monitor page displays a list of the files waiting to finish workflow steps. It displays an item for each file and each unfinished step in the workflow; a file may have multiple entries, depending upon what step in the workflow has been completed.

For each file, the following information becomes available:

Barcode	Barcode of array.			
Array Name	Name assigned to the array by the user.			
Probe Array Type	Model of probe array.			
Sample file	Name of Sample file.			
Workflow Step	The uncompleted step in the workflow.			
Project	Project folder the Sample file is assigned to.			
Status	Running.Not Ready.Frror.			

Sorting the file list by any column

1. Click on the column's header.

Networking



Network functionality

A computer running, GCC can be connected to a Windows network to provide the following functions:

Using network data storage

If the Windows network has a network data root, you can consolidate data from multiple computers running GCC Instrument Control in a single location. GCC Portal provides convenient ways to keep Sample (ARR) files and data files (DAT and CEL) in the same folder on the network data storage.

Running different parts of the workflow on different IC workstations In some cases the Fluidics Station and Scanner used to process an array are controlled by different workstations. GCC software enables you to perform different workflow tasks on different workstations while consolidating the Sample (ARR), Data (DAT and CEL) and Audit files at a single storage location (during processing the files may be on different machines).

Examples of different configurations for GCC with Windows network are given in "Sample configurations for GCC with network functionality" on page 339. Contact your IT/CIS support for help with configuring network functionality.

After installing the GCC components, to use the network functionality you need to:

1. Connect the computer to a Windows network with necessary permissions and have permissions set for using network data storage.

See "Setting up Windows networking" on page 343 for more information.

2. Configure GCC Services with the proper domain and user account with password to access the network assets.

See "Configuring GCC services" on page 344 for more information.

3. Add network data storage as a data root in GCC Portal

"Adding the network data storage as a data root" on page 347.

Sample configurations for GCC with network functionality

This section describes some sample configurations using GCC network functionality:

- "Linked instrument control systems"
- "Network storage" on page 341

The sample configurations show some of the ways you can connect computers with different roles in order to consolidate data, perform different parts of the workflow, and provide data access to other users.

Linked instrument control systems This configuration (Figure 406) enables you to perform different instrument control tasks on different workstations while consolidating the data files on the Scanner workstation.



In the linked IC Workstation configuration, the Scanner Workstation and the GCC Fluidics Workstation are linked with Windows Network.

Computer roles in
linked control
systemsScanner systemThe scanner workstation can be considered the 'main' system, in that the Sample files
will be generated and stored there and all related DAT, CEL, and CHP files can be
consolidated at the same location.The dataroot of the scanner workstation is shared so that the fluidics workstation can
access the Sample files and log AUDIT information for the arrays that are run through
the fluidics station, without needing to copy the files locally.

Requirements for the scanner system:

- Has the following software installed
 - Windows 10 Enterprise 2016 LTSB
 - GCC Portal with GCC Portal Web Server
 - GCC Viewer
 - GCC Scanner Control

Tasks that can be performed using the IC Scanner Workstation:

- Create and edit Sample (ARR) file and Register Array
- Run Scan on array to create DAT file
- Grid and get CEL Data (and perform manual grid alignment check if necessary)
- Index and search the workstation data.

Fluidics system

In the linked system, the fluidics workstation does not store any Sample files, or generate DAT, CEL or CHP files. It uses the Sample files on the scanner system, and writes back AUDIT information about the fluidics processing. If necessary, the fluidics workstation can also register arrays/samples that will be stored on the scanner workstation.

The IC workstation has GCC Portal and GCC Instrument Control installed. A Fluidics workstation can control up to eight fluidics stations.

Requirements:

- Has the following software installed
 - Windows 10 Enterprise 2016 LTSB
 - GCC Portal with GCC Portal Web Server.
 - GCC Fluidics Control
- Connected through Windows Network to the Scanner System.
- Have necessary Domain and User Permissions settings to enable Read/write to the Scanner System.
- GCC Services configured to work with Scanner System.
- Have Scanner System set up as a data root for GCC Portal

Tasks that can be performed using the IC Fluidics Workstation:

- Run Fluidics station and update the Audit file for the array.
- Index and search the Fluidics workstation data and the Scanner workstation data.
- Edit Sample (ARR) files on the Scanner and Fluidics workstation data.

The Fluidics system can also move data to and from Scanner System using Windows Explorer.

A

Network storage This configuration (Figure 407) provides storage and tools to consolidate the data produced by a set of IC workstations. It also enables other users linked through the Windows Network system to access the data.



Computer roles for network storage

The network data storage configuration supports the following computer roles:

- "Network data storage"
- "GCC IC workstations"
- "Local analysis workstation"
- "Local lab computer"

Network data storage

Network data storage serves as the central data repository for the networked computers. Sample (ARR) files are created on it and the DAT and CEL data are pushed out to it from the IC workstations. The network data storage computer does not need to have any GCC software installed.

GCC IC workstations

The IC workstation has GCC Portal and GCC Instrument Control installed. An IC workstation can control one scanner and up to eight fluidics stations.

GCC IC Workstations have the following requirements:

- Has the following software installed
 - Windows 10 Enterprise 2016 LTSB
 - GCC Portal with GCC Portal Web Server
 - GCC Viewer
 - GCC Instrument Control
- Connected through Windows Network to the network data storage.
- Have necessary Domain and User Permissions settings to enable Read/Write access to the network data storage.
- GCC Services configured to work with network data storage.
- Have network data storage set up as a data root for GCC Portal.

Tasks that can be performed using the IC Workstation:

- Create Sample (ARR) file and Register Array on network data storage and the workstation.
- Run Fluidics and Scan array to create DAT file.
- Grid DAT files, perform manual grid alignment check if necessary, and generate CEL file data.
- Use GCC Portal data management functions to upload DAT and CEL files to network data storage in same folder as Sample (ARR) file.
- Index and search the network data storage and the workstation data.
- Edit Sample (ARR) files on the network data storage and the workstation.

Note: The local IC workstation can also move data to and from network data storage using Windows Explorer.

Local analysis workstation

The IC workstation has GCC Portal and GCC Viewer installed.

A local Analysis Workstation has the following requirements:

- Windows 10 Enterprise 2016 LTSB
- GCC Portal with GCC Portal Web Server.
- GCC Viewer
- Connected through Windows Network to the network data storage
- Have necessary Domain and User Permissions settings to enable Read/Write access to the network data storage.
- GCC Services configured to work with network data storage.
- Have network data storage set up as a data root for the GCC Portal

It can perform the following tasks:

- Create and edit Sample (ARR) files on the network data storage and the workstation.
- Index and search the network data storage and the workstation data.
- Manual Gridding of DAT files on the workstation.
- Re-calculating CEL file data after gridding.

The local Analysis Workstation can also move data to and from network data storage using Windows Explorer.

Local lab computer

Lab Computers do not have any GCC software installed. Lab Computers are commonly used to perform higher-level analysis on the data.

Requirements:

- Connected through Windows Network
- Have necessary Domain and User Permissions settings to enable Read/Write access to the network data storage.

The local Lab computer can move data to and from network data storage using Windows Explorer.

Setting up Windows networking

A computer running GCC can be connected to a Windows network to provide different options for data consolidation and sharing.

Computers connected to the network are organized into domains. A domain is a group of computers that share common security and user account information.

Each user is assigned to a domain and given a user account with a name and password.

Any computer on the proper domain with necessary user permissions can get on the system using Windows Explorer and move data files on and off the network data storage.

If on a Windows domain these need to be domain accounts. If not on a Windows domain the share and the machine need matching account names and passwords.

Work with your IT department for help in setting up the necessary domain and user accounts.

If the domain, user account, and permissions are correct, when the computer running GCC is connected to the network you should be able to see the network data storage using Windows Explorer. You will not be able to add network data storage as an GCC data root or use GCC Portal to search the network data storage until you have configured the GCC Services with the proper domain and account information.

Sharing and security

You can use the Windows Sharing and Security settings to control access to your data when using network functionality. GCC supports setting permissions at the folder level, not the file level, even though the Windows settings can be set at the file level. You can change the settings for Sharing, permissions, and security for a selected file, but you need to be very careful about setting permissions when using GCC; you could lock yourself out of your own data or deny access to other people if the permissions are set incorrectly.

Work with your IT department for help in setting the permissions.

Examples

Let's take two different examples of how you might configure your file permissions for a network folder.

In the first example, you have a folder that is shared by your department. This folder enables read and write access to a Windows domain group called "Liver Cancer Group", and grants no other permissions to anyone else. In order for GCC to be able to access this network folder, you must change your GCC Services to run as one of the users who is a member of the Liver Cancer Group.



In the second example, you have a folder on a computer in a lab that you want access to, but you don't want anyone else to access that folder. If you create a local user account on that computer called LocalUser, with the password "LocalPassword", then, you can share that folder on the network, but grant access only to LocalUser. If you have a computer outside of that lab that has GCC installed, then you can also create LocalUser as a local user on this second computer, with the same password, and then change the GCC services on that second computer to run as LocalUser. Now, if you add your network folder as a Data Root, then you should be able to have complete access to that network folder in GCC.

Configuring GCC services

GCC services are tools that perform the functions of the software. To add a network data share as a data root, these services need to be configured as a domain user account, instead of a local system account.

The GCC services that need configuring include:

- GCCAuditLogger
- GCCIndexer
- GCCTaskManager
- GCCWebServer
- GCC96FS_WorkflowSvc

If on a Windows domain these need to be domain accounts. If not on a Windows domain the share and the machine need matching account names and passwords.

Note: You can use matching local accounts on a domain, but you need to be logged in using an account with Administrator privileges to perform this configuration.

Configuring the GCC portal services

- From the Start menu, click Control Panel → Administrator Tools. The Control panel opens.
- 2. Double-click the **Services** icon.

The Services window opens.

There are five GCC Services:

- GCCAuditLogger
- GCCIndexer
- GCCTaskManager
- GCCWebServer
- GCC96FS_WorkflowSvc

You will need to perform steps 3 through 6 for all services.

3. Right click **GCCAuditLogger** (or another service you are configuring) and select Properties.

The Properties dialog box opens.

- 4. Click the **Log On** tab.
- 5. Change the log on information for the service.
 - a. Change the service to Log on as "This account".

- Supply a domain user and password if on a domain.
- Supply a local account with matching username and password as the network storage device if not.
- b. Click OK.
- 6. Stop and start the service from the services dialog.
- 7. Repeat steps 3 through 6 for the other GCC services.

Configuring the GCC portal services

- From the Windows Start menu, click Windows System → Control Panel. The All Control Panel Items window opens.
- 2. Make sure the **View by** (upper right) is set to **Small icons**, then click on **Administrative Tools**.

The Administrative Tools window appears.

3. Locate, then double-click Services.

The Services window opens (Figure 408).

Figure 408	Services window					
🔍 Services					- 0	×
File Action View	v Help					
(+ +) 🖬 🗎	a 🗟 🔽 📷 🕨 🔳 💵 🕨					
🔍 Services (Local)	Services (Local)	_				
	GCC Audit Logger Service	Name	Description	Status	Startup Type	Log ^
	Stop the service Restart the service Description: GCC Audit Logger Service	 Downloaded Maps Manager Embedded Mode Encrypting File System (EFS) Enterprise App Managemen Extensible Authentication P Extensible Authentication P Fax File History Service Function Discovery Provide Function Discovery Resourc GCC Audit Logger Service GCC Indexer Service GCC Indexer Service GCC Audit Logger Service GCC Audit Logger Service GCC Make Service GCC Didexer Service <li< th=""><th>Windows se The Embed Provides th Enables ent The Extensi Enables you Protects use The FDPHO Publishes th GCC Audit GCC Audit GCC Indexe GCC Task M GCC Web S This service The service Makes local Performs ne</th><th>Running Running Running Running Running Running Running Running</th><th>Automatic (1 Automatic (0 Manual (Trig Manual (Trig Manual Manual Manual Manual Automatic Automatic Automatic Manual (Trig Automatic (1 Manual Manual (Trig</th><th>Net Loc Loc Loc Loc Loc Loc Loc Loc Loc Loc</th></li<>	Windows se The Embed Provides th Enables ent The Extensi Enables you Protects use The FDPHO Publishes th GCC Audit GCC Audit GCC Indexe GCC Task M GCC Web S This service The service Makes local Performs ne	Running Running Running Running Running Running Running Running	Automatic (1 Automatic (0 Manual (Trig Manual (Trig Manual Manual Manual Manual Automatic Automatic Automatic Manual (Trig Automatic (1 Manual Manual (Trig	Net Loc Loc Loc Loc Loc Loc Loc Loc Loc Loc
		Human Interface Device Ser HV Host Service Hyper-V Data Exchange Ser	Activates an Provides an Provides a		Manual (Trig Manual (Trig Manual (Trig	Loc Loc Loc Y
	Extended Standard					

- GCC Services:
 - GCCAuditLogger
 - GCCIndexer.
 - GCCTaskManager
 - GCCWebServer
- **GCC WorkflowBroadcastService**: This service enables the instrument to notify analysis applications that data is available for analysis.

- **GCC DeepLaserService**: This service enables the instrument to send notifications and upload data to the Thermo Fisher Scientific Cloud.
- 4. Right-click GCC Audit Logger (or another service you are configuring) and select Properties.

The Properties dialog box appears. (Figure 409)

5. Click the **Log On** tab.

Figure 409 Properties	GCC AuditLogger dialog box, Log On tab
General Log On Re	covery Dependencies
Log on as:	
Local System acco Allow service to	unt interact with desktop
This account:	ppavic Browse
Password:	•••••
Confirm password:	•••••
Help me configure use	er account log on options,
	OK Cancel Apply

- 6. Change the log on information for the service.
 - a. Change the service to Log on as "This account".
 - b. Supply a domain user and password if on a domain.
 - c. Supply a local account with matching username and password as the network storage device if not.
- 7. Click **OK**.

A message window appears stating you have been granted Log On As privileges.

8. Click OK.

A message window appears stating you must stop and restart the service to initiate your new login appears.

9. Click **OK**.

The Services window appears.

- 10. Click to highlight the service you just modified. then **Stop** and **Start** the service from the services dialog.
- 11. Repeat steps 4 through 10 for each remaining GCC service.



Adding the network data storage as a data root in GCC Portal

- 1. Start GCC Portal.
- 2. Navigate to **Data** \rightarrow **Data Roots** \rightarrow **Add**.
- Paste the UNC path to the share into the dialog box. UNC paths follow this format: \\servername\share. Mapped network drives should not be used (mapped network drives are network folders that a user has mapped to a drive letter, for example, "H:".)

Figure 410 Adding network	data root		
Search Files By: 🖾 Array	Name RATION HELP	(Use * for wildcard) 2 <u>Advanced Search</u>	۹
Add Data Root⊠			
Data Roots → C:\Command_Console\Data Available folders G: → Wy Documents B:- ← C:\	New data root	etrix.com\shares\SantaClara\Personal\rallso\Command_Console\Data	Add

4. Click Add.

Note: If you have not configured the GCC Services correctly, you will see a warning message in the Add Data Root window. For more information on, see "Configuring GCC services" on page 344

If you configured this correctly you should be able to view the share in the Folder Viewer.

Figure 411 Network data root				
Search Files By: Array Name (Use * for wildcard) Advanced Search (Use * for wildcard)				
Folders G-fill\shares\SantaClara\Personal\ G-fill_P-Dr Holmes Lab [Dr Holmes]	Current Folder: \\shares\Santal Open Add Subfolder	Clara\Personal\rallso\Command	l_Console\Data\Dr H	Iolmes Lab 📓
H-Alzheimer [Alzheimer 1, Dr Holmes] H-Cancer [Dr Holmes] Command_Console\Data	View New_View V Custom 2 Folders, 23 Files, 0 Selected	Select All Unselect	Custom	Nun <select a="" command=""></select>
	Selected File Name	Project Lot Name Number	on <u>Array Name</u>	Array Folder
	کیں ۰۰	Alzheimer 1, Dr Holmes		
	Cancer	Dr Holmes Dr Holmes	abcde	\\shares\SantaClara\Personal\rallso\Comma Holmes Lab
	fghii.ARR	Dr Holmes	fghij	\\shares\SantaClara\Personal\rallso\Comma Holmes Lab
	GCOS 1.3.ARR	Dr Holmes Dr Holmes 3000048	GCOS 1.3 GCOS 1.3	I (snares (santaciara) Personai (raliso (Comma Holmes Lab I (shares (santaCiara) Personal (raliso) Comma Holmes Lab



Windows sharing and security issues

You can use the Windows Sharing and Security settings to control access to your data when using network functionality. GCC supports setting permissions at the folder level, not the file level, even though the Windows settings can be set at the file level. You can change the settings for Sharing, permissions, and security for a selected file, but you need to be very careful about setting permissions when using GCC; you could lock yourself out of your own data or deny access to other people if the permissions are set incorrectly.

Note: Contact your IT/CIS support for help in setting the permissions for folders and files.

The Windows file sharing and security issues are described in further detail in:

- "General principles of security in the Command Console software", below
- "How do files get permissions that do not match the folder?" on page 349
- "How does Command Console show this error?" on page 349
- "How to avoid this issue" on page 349
- "How to adjust permissions for files in a folder" on page 350

General principles of security in the Command Console software

Security within Command Console can be separated into two different functional areas:

- Viewing file lists in the web UI, either from folders or from search results.
- File operations, such as editing or creating.

Security for viewing file lists is implemented at the folder level. If a user has read permissions on a particular folder, Command Console will not display files within that folder if the user does not have read permissions for those files. In addition, if the user tries to perform various operations on those files, the operating system will not allow it. Conversely, if the user has read permissions to several files in a folder, but does not have read permissions on the parent folder, the files will not be displayed in the Command Console software. In order to maintain consistent permissions on files within the system, individual files should not have permissions set differently from their parent folder. If this occurs due to other applications or operating system functions, the permissions on all the files in a folder can be reset by an administrator.

When performing file operations, including editing the Sample (ARR) file, re-gridding the Image (DAT) file, or regenerating an Intensity (CEL) file, a user may be prohibited by the operating system if the user does not have appropriate permissions for that file. The Command Console UI attempts to indicate when an operation fails due to permissions, but there are times when the operating system does not indicate why an operation failed. If the user e10ects to be able to modify a file but cannot, and can modify other files within the same folder, it is possible that individual files have permissions that limit access. If this occurs, the file permissions should be checked by an administrator and reset as necessary.

B

Llow do filos cot	
permissions that do not match the folder?	Under most operating conditions, the files in a folder will have the same permissions as the folder in which they reside. However, there are particular cases when a file is moved that may cause the file to retain certain permissions that were applied to the file in its previous location. In this case, the file will not have the same permissions as the new folder or the other files in the folder.
	This happens to files that are moved to a new folder on the same NTFS partition on a local hard disk. It is important to note - this is a function of the Operating System, not Command Console.
	As an example, a data folder has two subfolders, Project1 and Project2, and the Project1 and Project2 folders have different permissions. If a user with appropriate permissions moves a file from Project1 to Project2, the files moved to the Project2 folder may retain some of the permissions applied in the Project1 folder. If another user who has permissions to the Project2 folder but not to the Project1 folder tries to perform operations on these moved files, the operations may fail.
	There are many conditions where this does not occur:
	• Moving a file from a local hard disk to network storage (C:\data to \\storage\data)
	 Moving a file from one folder to another on network storage (\\storage\data to \\storage\backup)
	 Moving a file from one local hard disk to another local hard disk (C:\data to D:\data)
	Copying files from one location to another
How does Command Console show	The files or folders to which the user does not have access are not visible in the GCC Portal pages. For example, if the user has read permission for a folder, but is denied access to specific files in the folder, then the following files are not displayed on the following pages:
	Folder View
	Search Results
	Project View
How to avoid this issue	There are ways to avoid this issue that will not impact normal operations. These include:
	 Not setting overly restrictive permissions on shared systems, especially Instrument Control Workstations
	 Using network storage for the bulk of data, and applying permissions on the network folders
	Only applying permissions on the network folders that are truly necessary
	Access data through UNC paths whenever possible

Security recommendations

- Set permissions for groups, as opposed to individuals, for greater simplicity.
- Only restrict permissions to the degree needed, again for greater simplicity.
- Set permissions at the folder level when creating data roots and projects.
- Don't use Deny permissions unless absolutely necessary, as these are more likely. to cause a situation with conflicting entries.
- Don't restrict (deny) the "Read permissions" permission. This is needed in order for the software to properly determine the rights the user has for a given object.
- Take care when moving files that the consistency is not broken. If possible, move files by using the WebUI Copy Project and Upload Data functions.
- When permissions do get out of sync, they can be easily restored by an admin, who can remove the conflicting ACL entries and allow the file to get its permissions by pure inheritance.

How to adjust permissions for files in a folder

- To reset the permissions for all files and sub-folders in a folder:
 - Right-click on the folder in question and select **Properties.** The folder's Properties dialog box appears.
 - 2. Click the Security tab. (Figure 412)



3. Click the Advanced button.

The Advanced Security Settings dialog box opens. (Figure 413)

gure 413	3 Advanced Setting	s tab						
Advanced Se	ecurity Settings for Command_C	onsole		– o >				
Name:	C:\Command_Console							
Owner:	SYSTEM 🛛 🗣 Change							
Permissions	Auditing Effective A	Auditing Effective Access						
ermission er	ntries:	Δ <i>ε</i> ερες	Inherited from	Applies to				
	Administrators (MCGTOWIN1	Full control	C·\	This folder, subfolders and files				
Allow	SYSTEM	Full control	C:\	This folder, subfolders and files				
Allow	Users (MCGTOWIN10IOT\Users	Read & execute	C:\	This folder, subfolders and files				
Allow 🤱	Authenticated Users	Modify	C:\	This folder, subfolders and files				
🗣 Change j	permissions View							
Disable inh	heritance							

- 4. Verify that the security settings are appropriate.
- 5. Click to select (highlight) the permission entry you want to modify, then click **Change permissions**.

The following permission options appear. (Figure 414)

lame:	C:\Command_Console						
)wner:	SYSTEM Change						
Permissions	Auditing Effective Access						
Type	Principal	Access	Inherited from	Applies to			
Type	Principal	Access	Inherited from	Applies to			
10	A. L. S. S. A. MAGGTOMMAN	E 11		TI C C C C C C C C C C C C C C C C C C C			
Allow Allow	Administrators (MCGTOWIN1 SYSTEM	Full control Full control	C:\ C:\	This folder, subfolders and files This folder, subfolders and files			
Allow Allow Allow	Administrators (MCGTOWIN1 SYSTEM Users (MCGTOWIN10IOT\Users)	Full control Full control Read & execute	C:\ C:\	This folder, subfolders and files This folder, subfolders and files This folder, subfolders and files			
Allow Allow Allow Allow Allow	Administrators (MCGTOWIN1 SYSTEM Users (MCGTOWIN10IOT\Users) Authenticated Users	Full control Full control Read & execute Modify	C:\ C:\ C:\	This folder, subfolders and files This folder, subfolders and files This folder, subfolders and files This folder, subfolders and files			

6. Click the appropriate button and click the **Replace all child object permission entries...** check box (if applicable), then click **OK**.

The following notice may appear. (Figure 415)

Fig	ure 415 Security notice box
1	This will remove explicitly defined permissions on all child objects and enable propagation of inheritable permissions to those child objects. Only inheritable permissions propagated from Data will take effect. Do you wish to continue?

To replace the permission you just modified, click Yes.

Note: This will reset the permissions for all files and sub-folders of the selected folder.



Cell summary report

Report description

The Cell Summary Report is a tool for monitoring the performance of the hybridization and grid alignment of arrays. The report enables you to detect problems in these steps and compare the performance of different chips.

The Cell Summary Report uses the control features on the array. Control features are cells with special probes; the corresponding targets are spiked into the sample cocktail. The resulting patterns of bright and dark cells are used in grid alignment and other processes.

In GCC the Cell Summary Report is automatically generated when CEL files are generated for certain types of arrays. These arrays require a GRC file in the library file set. If you generate a CEL file for one of these arrays and the GRC file is not available, you will see an error notice.

You can learn more about the Cell Summary reports in the following sections:

- "Report description"
- "Using the cell summary report" on page 358
- "Cell summary report algorithm" on page 359

The cells that failed the analysis can be seen in the GCC Viewer when looking at the DAT or CEL file (see "File display differences" on page 276).

The reports are placed in the data root and subfolder with the CEL file.

The cell summary report components are described in "Cell summary report Components for non-re-sequencing chips".

The Cell Summary Reports for all types of chips except Resequencing (Expression, Mapping, and others) provides information on the following features:

- Non-synthesized features
- OligoB1 features
- OligoB2 features

Refer to the relevant manual for the GeneChip array for more information about these features.

Opening the Cell Summary Report

- 1. Open the CEL file in the GCC Viewer.
- 2. In the Properties box, click on the Report row.

A button appears in the Report Row. (Figure 416)

3. Click on the button to open a text display of the CELL Summary report.

Cell summary report Components for non-resequencing chips



File View Help					
逽 Search & Open	🚰 Open File 📙 Save	🕜 Help			
Properties	д X	. 8 @5200440	06626140111074017	56875981.CEL	4 ۵
				031 23	
	9bd97756ddd44aa4.a0			Patricipation and a second	(Construction)
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Barcode	@52004400662614011			(1) A state of the state of	Construction of the
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Cel					
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Maximum Intensity	65534				
Minimum Intensity	1				A state of the second stat
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X Remove Selected	😰 Refresh 🛛 Please dou	uble click an item to open	it.		
	Name	Array Type	Date Reviewed	Grid Alignment	CEL Generat
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Date Scanned 6/21/2007 11:47: 6/26/2007 12:44: 6/26/2007 12:48:	0 Subject_03_brain_2.D 4 Subject_03_brain_3.D 3 Subject_01_brain_2.D)AT HuEx-1_0-st-tai)AT Test3	1 7/24/2007 8:31:43 Al 7/17/2007 3:17:09 Pl	M Failed: Failed t M Passed	Not Available Passed
Date Scanned 6/21/2007 11:47: 6/26/2007 12:44: 6/26/2007 12:48: 6/26/2007 12:48:	0Subject_03_brain_2.D :4Subject_03_brain_3.D 3Subject_01_brain_2.D :4Two_Arrays_U133A_2	DAT HuEx-1_0-st-ta DAT HuEx-1_0-st-ta DAT Test3 2_2 HG-U133A_2	1 7/24/2007 8:31:43 Al 7/17/2007 3:17:09 Pl 7/23/2007 4:47:58 Pl	M Failed: Failed t M Passed M Passed	Not Available Passed Passed
Date Scanned 6/21/2007 11:47: 6/26/2007 12:44: 6/26/2007 12:48: 6/26/2007 1:14:5 6/26/2007 1:14:5	0 Subject_03_brain_2.D 4 Subject_03_brain_3.D 3 Subject_01_brain_2.D 4 Two_Arrays_U133A_2 4 Two_Arrays_U133A_2	DAT HuEx-1_0-st-ta DAT Test3 2_2 HG-U133A_2 2_1 HG-U133A	1 7/24/2007 8:31:43 Al 7/17/2007 3:17:09 Pl 7/23/2007 4:47:58 Pl	M Failed: Failed t M Passed M Passed Passed	Not Available Passed Passed Passed
Date Scanned 6/21/2007 11:47: 6/26/2007 12:44: 6/26/2007 12:48: 6/26/2007 1:14:5 6/26/2007 1:25:3 6/26/2007 1:26:4	0 Subject_03_brain_2D 4 Subject_03_brain_3D 3 Subject_01_brain_2D 4 Two_Arrays_U133A_2 4 Two_Arrays_U133A_2 7 Subject 01 brain 3D	AT HuEx-1_0-st-ta AT HuEx-1_0-st-ta DAT Test3 2_2 HG-U133A_2 2_1 HG-U133A DAT Test3	1 7/24/2007 8:31:43 Al 7/17/2007 3:17:09 Pl 7/23/2007 4:47:58 Pl	M Failed: Failed t M Passed M Passed Passed Passed	Not Available Passed Passed Passed Passed
Date Scanned 6/21/2007 11:47. 6/26/2007 12:44. 6/26/2007 12:48. 6/26/2007 11:45. 6/26/2007 11:26:4 7.12/2007 10:11.	0 Subject_03_brain_2.D 4 Subject_03_brain_3.D 3 Subject_01_brain_2.D 44 Two_Arrays_U133A_2 44 Two_Arrays_U133A_2 7 Subject_01_brain_3.D 	AT HuEx-1_0-st-ta)AT HuEx-1_0-st-ta)AT Test3 2_2 HG-U133A_2 2_1 HG-U133A)AT Test3 (320 E = 5 2	1 7/24/2007 8:31:43 Al 7/17/2007 3:17:09 Pl 7/23/2007 4:47:58 Pl	M Failed: Failed t M Passed Passed Passed Passed	Not Available Passed Passed Passed Passed Passed
Date Scanned All 6/21/2007 11:47. 6/26/2007 12:44. 6/26/2007 12:48. 6/26/2007 12:48. 6/26/2007 12:48. 6/26/2007 12:53. 6/26/2007 12:53. 6/26/2007 12:54. 7/13/2007 10:11: 7/13/2007 10:11.	0 Subject_03_brain_2.D 4 Subject_03_brain_3.D 3 Subject_01_brain_2.D 4 Two_Arrays_U133A_2 4 Two_Arrays_U133A_2 7 Subject_01_brain_3.D 1 @5113020045754400	HuExt_0st of HuExt_0st of HG-U133A_2 2HG-U133A_2 2_1HG-U133A HG-U133A DAT Test3 6130E_coli_2	1 7/24/2007 8:31:43 Al 7/17/2007 3:17:09 Pl 7/23/2007 4:47:58 Pl	M Failed: Failed t M Passed M Passed Passed Passed Passed	Not Available Passed Passed Passed Passed Passed

The Text Editor opens with the Cell Summary Report displayed. (Figure 417)

Figure 417 Cell	Summary report for Non-resequencing array	
Report Header	Report Cell Summary Report Date: Wed Jul 25 03:23:17 2007 Filename: @65200440066261401107401756875981.CEL GRC Filename: Mapping50K, Hind240 grc Probe Array Type: Mapping50K_Hind240	
Report Summary	Summary Foilures Total Failure Rate Non-synthesized features: 3 5588 0.1% Bright control probes: 0 8641 0.0% Dim control probes: 5 8803 0.1% Total control features: 8 23032 0.0%	
Metrics	Intensity threading of the non-synthesized features: 715,0 Median intensity of bigg82: 61775,0 Median intensity of bigg82: 61775,0 Median intensity of bigg81: 623,0 Number of non-synthesized features that were expected to be dim but were not: 3 Number of probes that were expected to be dim but were not: 5 Total number of non-synthesized features on the array. 5588 Total number of non-synthesized features on the array. 5588 Total number of available dim probes on the array. 8603 Total number of available dim probes on the array. 8603 Total number of available dim probes on the array. 8603 Total number of available dim probes. 53544.2 Average intensity of the dim probes. 365.1 Total Grid Failures : 8 805	
	Can	cel

This report contains the following sections:

- "Report header"
- "Summary" on page 355
- "Metrics" on page 356

Report header

Figure 418	Expression Cell Summary report: header
Report Type:	Cell Summary Report
Date:	Wed Jul 25 03:23:17 2007
Filename:	@52004400662614011107401756875981.CEL
GRC Filename:	Mapping50K_Hind240.grc
Probe Array Typ	e: Mapping50K_Hind240

The report header (Figure 418) lists basic information about the Cell Summary report:

Report Type	Used to distinguish types of reports (Cell Summary Report, Algorithm Report, etc.).
Date	Time and date report was generated.
Filename	Input CEL data file name that was used to generate the report.
GRC Filename	Name of the GRC file used to generate the report.
Probe Array Type	Array type used for the CEL file.

Summary

Figure 419	Expression Cell Summary report: Summary

Summary						
Name and the strend for the second	Failures		l otal		Failure R	ate
Non-synthesized reatures:	3	~	2266	00.44	0.1%	0.00
Bright control probes:	_	U		8641		0.0%
Dim control probes:	5		8803		0.1%	
Total control features:		8		23032		0.0%

The Summary (Figure 419) displays information:

For the following types of features:

Non-synthesized features

Bright control probes

Dim control probes



Total control features

The summary lists the following values:

Failures	The number of features in the category that failed.
Total	The total number of features in the category.
Failure Rate	The percentage of features in the category that failed.

Metrics

Figure 420 Expression Cell Summary report: metrics	
Intensity threshold: Median intensity of the non-synthesized features: Median intensity of oligoB2: Median intensity of oligoB1: Number of non-synthesized features that were expected to be dim but were not: Number of probes that were expected to be bright but were not: Number of probes that were expected to be dim but were not: Total number of probes failing the threshold test: Total number of non-synthesized features on the array: Total number of available bright probes on the array: Total number of available dim probes on the array: Total number of available probes on the array: Average intensity of the bright probes: Average intensity of the dim probes:	7159.6 714.0 61775.0 829.0 3 0 5 8 85588 8641 8803 23032 59544.2 965.1
Total Grid Failures : 8	

The metrics section (Figure 420) displays additional data about the B1 and B2 oligos.

Failed cell locations

Figure 421	Cell intensity of	data with	failed co	ontrol features	masked	
File View Help						
 Search & Open	🚰 Open File 🔛 Sa	ave 🛛 🕜 Help				
Properties	д	× 🛛 🗑 @	520044006	62614011107401756	875981.CEL	4 6
₽∎ ¢ ↓ 🔤		ি চৰ 🔍	QQI	🔲 🙆 I () I 🗈	0 <) > <	
Array Information	•				and the second	Constanting of
Array ID	9bd9775f-ddd4-4ae4-a		SACE 1	1000 Car # 1	11.24440	6-15-10-
Array Name		ACCESS OF		Program and the second second		网络白根
Barcode	@5200440066261401	1 10000	36.9	360.071	1.11.128.12	101220
DAT File Name	C:\Command_Console	C. Provide	1999 A		1993 - BANK 19	References.
Design Type	Mapping	and the second		- All Street	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1.1104.0
Probe Array Type	Mapping50K_Hind240	- Capita		ALC: NOT THE OWNER.	ALC: NO DOM: N	10000
Cel			1996 - N	AND REPORT	enter de la fille	1.000
Cel Columns	1600	- Charles	1000	States 197	1. A 10 10 10 10	e e contra d
Cel Hows	1600			and provide the state	10.000 A.C.	A 1997
File Version	10000033726-1185358	- Para	1	an a	CARD IN A PROPERTY OF	Service Service
Folder Location	C:\Command_Console'		1000	COLUMN TWO IS NOT	The second second	700.000
Maximum Intensitu	65534				and the second second	10 M M M M
Minimum Intensity	1	1 1 2 2 2 2 2	200 B	We Wanter Ma	1890 C 1894	Fight Party
Modified Date	7/25/2007 3:23:17 AM	 C2000 	trabér,	ALC: NOT THE OWNER.	by the last	122.000
Cel Summary Re	port	i lente	200	- 200 Marine da		Constant of the
Bright features	0	110,00			CONF. INC.	E. (1996)
Dim features	5	10.146	6-19-19.	and the Solid of	cancel of	10.00
Non-synthesized fea	a 3	1955.0	1.14			- 10 C
Report	Report Type: Ce		10.000	And States and	a third states	
- Huidics		1.000	100.000	20.402.0T	10.001563	activation of the
Fluidics Date		✓ <			(m)	>
Review						Д
Y Demove Selected	Pefrech Diesce	double click an its	em to open it			
Data Seamed	Name		su Tune	Data Reviewed	Grid Alignment	CEL Constatio
			аутуре			CEL Generatio
6/21/2007 11:47:	U Subject_U3_brain_	Z.DAT Hub	x-1_0-st-tal	772372007 4:51:38 PM	Failed: Failed t	Not Available
LINES A LOOP LOOP AND A TOTAL ST						
6/26/2007 12:44:	4 Subject_03_brain_	3.DAT Hub	x-1_0-st-ta1	7/24/2007 8:31:43 AM	Failed: Failed t	Not Available
6/26/2007 12:44: 6/26/2007 12:48:	4 Subject_03_brain_ 3 Subject_01_brain_	3.DAT Hub 2.DAT Tes	Ex-1_0-st-ta1 t3	7/24/2007 8:31:43 AM 7/17/2007 3:17:09 PM	Failed: Failed t Passed	Not Available Passed
6/26/2007 12:44: 6/26/2007 12:48: 6/26/2007 1:14:5	4 Subject_03_brain_ 3 Subject_01_brain_ 4 Two_Arrays_U133	3.DAT HuB 2.DAT Tes A_2_2 HG-	Ex-1_0-st-ta1 t3 -U133A_2	7/24/2007 8:31:43 AM 7/17/2007 3:17:09 PM 7/23/2007 4:47:58 PM	Failed: Failed t Passed Passed	Not Available Passed Passed
 6/26/2007 12:44: 6/26/2007 12:48: 6/26/2007 1:14:5 6/26/2007 1:25:3 	4 Subject_03_brain_ 3 Subject_01_brain_ i4 Two_Arrays_U133 4. Two_Arrays_U133	3.DAT Hub 2.DAT Tes A_2_2 HG- A_2_1 нG-	5x-1_0-st-ta1 t3 -U133A_2	7/24/2007 8:31:43 AM 7/17/2007 3:17:09 PM 7/23/2007 4:47:58 PM	Failed: Failed t Passed Passed Passed	Not Available Passed Passed Passed
6/26/2007 12:44: 6/26/2007 12:48: 6/26/2007 1:14:5 6/26/2007 1:25:3 0/26/2007 1:25:3	 Subject_03_brain_ Subject_01_brain_ Subject_01_brain_ Two_Arrays_U133 Two_Arrays_U133 	3.DAT Hub 2.DAT Tes A_2_2 HG· A_2_1 HG·	5x-1_0-st-ta1 t3 -U133A_2 -U133A	7/24/2007 8:31:43 AM 7/17/2007 3:17:09 PM 7/23/2007 4:47:58 PM	Failed: Failed t Passed Passed Passed	Not Available Passed Passed Passed
6/26/2007 12:44: 6/26/2007 12:48: 6/26/2007 1:14:5 6/26/2007 1:25:3 6/26/2007 1:26:4	4 Subject_03_brain_ 3 Subject_01_brain_ 4 Two_Arrays_U133 4 Two_Arrays_U133 7 Subject_01_brain_	3.DAT Hub 2.DAT Tes A_2_2 HG- A_2_1 HG- 3.DAT Tes	ix-1_0-st-ta1 t3 U133A_2 U133A t3	7/24/2007 8:31:43 AM 7/17/2007 3:17:09 PM 7/23/2007 4:47:58 PM	Failed: Failed t Passed Passed Passed Passed	Not Available Passed Passed Passed Passed
 6/26/2007 12:44: 6/26/2007 12:48: 6/26/2007 1:14:5 6/26/2007 1:25:3 6/26/2007 1:26:4 7/13/2007 10:11: 	4 Subject_03_brain_ 3 Subject_01_brain_ i4 Two_Arrays_U133 i4 Two_Arrays_U133 7 Subject_01_brain_ 1 ©5113020045754	3.DAT Huß 2.DAT Tes A_2_2 HG: A_2_1 HG: 3.DAT Tes 406130 E_c	5x-1_0-st-ta1 t3 U133A_2 U133A t3 t3 coli_2	7/24/2007 8:31:43 AM 7/17/2007 3:17:09 PM 7/23/2007 4:47:58 PM	Failed: Failed t Passed Passed Passed Passed Passed Passed	Not Available Passed Passed Passed Passed Passed
 6/26/2007 12:44: 6/26/2007 12:48: 6/26/2007 1:14:5 6/26/2007 1:25:3 6/26/2007 1:26:4 7/13/2007 10:11: 7/13/2007 10:14:5 	4 Subject_03_brain_ 3 Subject_01_brain_ i4 Two_Arrays_U133 i4 Two_Arrays_U133 Subject_01_brain_ Subject_01_brain_ 1 @5113020045754 3 @5200190030614	3.DAT Hu£ 2.DAT Tes 4_2_2 HG: 4_2_1 HG: 3.DAT Tes 406130 E_c 307020 HG:	5x-1_0-st-ta1 t3 U133A_2 U133A t3 t3 t0[_2 U133_Plu	7/24/2007 8:31:43 AM 7/17/2007 3:17:09 PM 7/23/2007 4:47:58 PM	Failed: Failed t Passed Passed Passed Passed Passed Passed	Not Available Passed Passed Passed Passed Passed Passed
 6/26/2007 12:44: 6/26/2007 12:48: 6/26/2007 11:4:5 6/26/2007 1:25:3 6/26/2007 1:26:4 7/13/2007 10:11: 7/13/2007 10:14:4: 	 Subject_03_brain_ Subject_01_brain_ Two_Arrays_U133 Two_Arrays_U133 Subject_01_brain_ Subject_01_brain_ @5113020045754 @5200190030614 	3.DAT Hu£ 2.DAT Tes A_2_2 HG A_2_1 HG 3.DAT Tes 406130 E_c 307020 HG	5x-1_0-st-ta1 t3 U133A_2 U133A t3 t3 t3 t0i_2 U133_Plu	7/24/2007 8:31:43 AM 7/17/2007 3:17:09 PM 7/23/2007 4:47:58 PM	Failed: Failed t Passed Passed Passed Passed Passed Passed	Not Available Passed Passed Passed Passed Passed Passed

Note: To view these probes on a DAT file, view the cell intensity display. For more information about this option, see "Viewing failed control features" on page 277.

Using the cell summary report

The Cell Summary report provides clues to problems in the fluidics, grid alignment, and other issues with the cell file.

It can be used to establish a baseline for performance, which can then be used for quality control for subsequent experiments.

Features can fail the evaluation due to sample and system issues such as:

- Incorrect gridding
- Incorrect concentration of control oligo in sample (too high or too low)
- Incorrect scanner arc correction
- Incorrect recording of the scanner pixel size
- Incorrect parameters for cell file generation
- Debris in the sample or on the array glass
- Array defects

Rules of thumb When processing a group of samples, identify the cell files that have the largest number of evaluation failures. This would be about ten percent of the cell files in the group. Use the graphic display described below to examine those cell files to identify any sample or system issues.

When processing one or two samples use the graphic display to examine those cell files with evaluation failures greater than ten.

In the event of substantial (greater than one hundred) evaluation failures the following guidelines may be helpful:

- Failures limited to mostly bright or mostly dim control probes usually indicate debris or array defects.
- Failures limited to mostly non-synthesized features often indicate non-specific binding and usually do not compromise any biological measurements.
- Failures spanning both bright and dim probes often indicate gridding, scanning or other systematic issues.

The relationship between Cell Summary Report results and biological results varies depending on the application. It is best to track these and determine trends for your laboratory and application.



Cell summary report algorithm

The algorithm's goal is to use the probe design information to identify all probes that should have high intensities and make sure they in fact have high intensities. Similarly with the probes that should be dim. The features that fail the evaluation are totaled and flagged to enable their graphic display.

Depending on the array/assay type, it is the target for the B1 probes that is spiked in and in others the target for the B2 probes is used.

Thus, the first step of the algorithm is to determine which of the two probe types is brighter overall. The median for each of the B1 and the B2 probes is determined and if there is sufficient contrast (difference in median intensities) the probe type with the larger median is taken to be the bright probe type.

If the contrast is insufficient an algorithm failure is reported. This kind of failure is typically only seen in the case of gross errors—such as use of the wrong library file, improper use of control reagents (spiking in both or neither of B1 and B2 control reagents) or rotation of the DAT image. The threshold is the calculated midpoint (or log midpoint) of the B1 and B2 medians.

The algorithm examines each feature. If the feature is either B1, B2, or nonsynthesized, then the intensity is compared against the threshold; otherwise, the feature is ignored. If the feature fails the threshold, then the feature is added to the total and the feature flagged to enable graphic display.



Installing library files and scripts

GeneTitan library file installer

 From the Launcher, double-click on GeneTitan Library File Installer. The GeneTitan Library File Installer window appears. (Figure 422)

Figure 422 GeneTitan Library File Installer				
🖼 appliedbiosystems - GeneTitan Library File Installer				
GeneTitan Library File Installer will extract the selected library files into the GCC library path				
Source Path:				Browse
Target Path:	Target Path: C:\Command_Console\Library			Browse
File Name	3	Path		
			Install	Close

2. Click the Source Path's Browse button.

A Browse For Folder window appears.

- 3. Navigate (as you normally would) to the source location of the library files you want to install.
- 4. Click Select Folder.

The available library file packages appear in the File Name and Path pane.

Note: Use the default Target path. Changing the target path is not recommended.

5. Click the check box(es) adjacent to the library filename you want to install, then click **Install**.

A progress bar appears.

After the installation is complete, an Installed successfully message appears.

6. Click **OK** to acknowledge the message, then close then the GeneTitan Library File Installer window.
- Ď
- 7. Enter the email account the messages will be sent from in the From box.
- 8. Enter the email account(s) to receive the message in the To... Box
- 9. Enter the SMTP Server and Port information in the appropriate boxes.
- 10. You can click the Test button to send a test e-mail.
- 11. Select the Scanner or Fluidics tab, depending upon which instrument you want to select messages for (Scanner or Fluidics).

The message list displays the messages you can select from. The messages correspond to different types of failures or other conditions in the instrument, as shown in Figure 423.

Figu	16 423	Message List for Scarin	ers
Scanner	Fluidics Da	ataUpload	
)	Subject	Body
3	32810	Scan error	Error while scanning.
3	32812	Scan error	Cannot read or create an array file
3	32813	Scan error	Cannot get the scan parameters for
3	32814	Scan error	This array has already been scar
3	33017	Scan error - Low disk space	Error while scanning. Not enough
3	33038	Door opened	The door was opened during a sc
3	33039	Scanner offline	The scanner network connection v
3	33040	Autoloader run started	The user listed in the email started
3	33041	Autoloader run complete	The autoloader run is complete.
3	33042	Chip loaded	A cartridge was loaded in the auto
3	33043	Scan started	A scan was started in the autoload
3	33045	Scan aborted	A user aborted a scan in progress
3	33046	Scan complete	The scan was completed.
3	33047	Rescan required	The autoloader door was opened
5	536900966	Scan error - cannot connect	Cannot connect to the scanner; ch
<			>

12. Select and edit messages:

- a. Select the check box next to the message ID.
- b. Click in the subject or body column for the message and edit the text.You can click the Default button to return to the original configuration.

13. Click **Save** to save the configuration changes.



Library file importer

Importing from CD or folders

1. From the Launcher, double-click on **Library File Importer**. The Library File Importer window appears. (Figure 422)



2. Click on the Import parameters from a GCOS library file package CD or folder radio button, then click **Next**.

The Select Source of Library Files window appears. (Figure 425)

Figure 425 Select Source of Library F	iles window
🚇 Command Console Library File Importer	– 🗆 X
Select Source of Library Files	
Select CD drive or folder location of source files to import	Browse
Select Save Location Location to save the Applied Biosystems GeneChip Command Conso	le library files:
C:\Command_Console\Lbrary	Browse
Çancel	<u>B</u> ack <u>N</u> ext

- Click the **Browse** button to select the drive location for files you want to import. The Browse for Folder window appears.
- 4. Navigate to your source location as you normally would, then click OK.
- 5. Click the **Browse** button, to select a saving location for files you are importing. The Browse for Folder window appears.

- 6. Navigate to your save location as you normally would, then click OK.
- 7. At the Library File Importer window (after your source and save locations are set), click **Next**.

The Select Probe Array Types window appears (Figure 426) and displays a list of the library files available in the selected folder or CD with their location. Duplicate probe arrays types are grouped at the top of the list.

Figure 426 Sele	ect Probe Array	Type wind	ow
Command Console Library File I	mporter	-	
Found all probe array types.			
Select Probe Array Types			
Probe Array Type	Location		
CytoScanOptima	Y^GCC library\CD_CytoSc Y^GCC library\CD_CytoSc	an HD_Picture Frame \Full\CytoS	CytoScanHD_ canOptima∖Li
<			
		Cancel Back	<u>S</u> tart

8. Click the appropriate check box or click **Select All**, then click **Start**. Click **Unselect All** to deselect your checked box(es).

A Status window (Figure 427) with a progress bar appears.

9. After processing has been successfully completed, click Finish.

Note: If you have selected the same library file from two sources, a warning appears. Click **OK** to return to the Select Array window, then deselect the duplicate array package. If you have selected library files that are already installed, a Choose Library Version window appears. Click the radio buttons to choose the appropriate versions, then click **OK**.

Figure 427	' Statu	s windov	v			
😨 Command Console	Library File Imp	porter		-		×
Processed all prob	e array types.					
Probe Array Type	Status	Message				
CytoScanHD_Array	Completed	Successfully import	ed			
Cyto ScanOptima	Completed	Successfully import	ed			
View Log			Import Others	Einish	Cano	sel



Fluidics script installer

 From the Launcher, double-click on Fluidics Script Installer. A Welcome window appears. (Figure 428)



2. Click Next.

The Select Software screen appears. (Figure 429)



3. Click Next.

The Select Directory window appears. (Figure 430)



Figure 430	Select Source window	
appliedbiosystems Flu	idics Script Installer – Select Directory	
Please select eith	er install from directory on file system or install from Thermofisher.com.	IN
 Install from director C:\Program Files (y on file system x85)\Affymetrix\Command Console	Browse
Install from Thermo	ofisher.com	
E-mailt		
Password		
	< Back Next >	Cancel

Installing from a directory

- 1. Click the radio button.
- 2. Click Browse.
- 3. Navigate to the file location as you normally would.
- 4. Click to select the protocol, then click **OK**.
- 5. The file location is now displayed.
- 6. Click Next.

The Select Package window appears. (Figure 431)

Installing from thermofisher.com

- 1. Click the radio button.
- 2. Enter your registered username (email) and password.
- 3. Click Next.

The Select Package window appears. (Figure 431)

Figure 431 Select	Package window	v
appliedbiograteme Eluidice Script Install	ar Salact Dackage	
applicubiosystems rutuics script installe	e – Select Package	6
Please select the package to be insta	alled and press the Next button.	TEM
List of valid packages	Fluidic Station	This package can be used to
FS450	FS450	with the Affymetrix FS 450 fluidics
		station. The package can be used
		Console Software or Affymetrix
		GeneChip Operating Software.
,		
	< Back	Next > Cancel

 Select the package you want to install, then click Next. The Select Protocols window appears. (Figure 432)

appliedbiosystems Fluidics Script	Installer – Select F	Protocols			
Please select the protocol(s) to	o be installed on the	e system and press the Ne	ext but	ton.	III
Protocol Name	New Version	Version of installed Scri	<u>^</u>	Select All	
CytoScan750K_Array_450	1	1		3	
CytoScanHD_Array_450	1	1		Clear	
CytoScanOptima_Array_450	1	1			
Cytogenetics_Array_450	1	1			
DMET_Plus_169_v2	1	1			
DNAarray_WS5_450	1	1			
EukGE-WS1v4_450	4	4			
EukGE-WS2v4_450	4	4			
EukGE-WS2v5_450	5.1	5.1			
FS450_0001	1.1	1.1			
FS450_0002	1.1	1.1			
FS450_0003	1.1	1.1			
FS450_0004	1	1			
FS450_0005	1	1			
FS450_0006	1.1	1.1			
F0450 0007		**	× I		
<		2			

 Select the check box(es) of the protocols you want to install, then click Next. The Summary window appears. (Figure 433)

Figure 433 Summary window	
appliedbiosystems Fluidics Script Installer – Summary The following is a summary of the package to be installed on the system.	
Selected Fluidos Script CytoScan750/CArey_450 CytoScan750/CArey_450 CytoScanOptima_Arey_450 CytoScanOptima_Arey_450 DNArary_X85 DNArary_WS5_450 EuKGE-WS1v4_450 EuKGE-WS1v4_450 EuKGE-WS2v4_450 EuKGE-WS2v4_450 EuKGE-WS2v4_450 EuKGE-WS2v4_450 EuKGE-WS2v4_50 FS450_0001 FS450_0001 FS450_0003 FS450_0005 FS450_0006 FS450_0006 GenromeWideSNP51_450 GenromeWideSNP5_450 Marcers 100/c1_1450	~
< Back Next >	Cancel

6. Review the information and click **Next**.

An Install window appears with a progress bar.

When the install is completed, the Finish window appears.

7. Click Close.

Note: If you opened the Installer through the GCC Fluidics Control Software, you must close the software, then reopen it for the installed scripts to appear in the drop-down lists.



Notification e-mails

Configuring notification e-mails

GCC provides e-mail notification of problems when:

- Running the GCS 3000 with AutoLoader
- Running the FS-450 Fluidics Station
- Running the GeneTitan Instrument
- Running the Data Uploader

You will need to get information on the SMTPPort and SMTPServer from your IT department.

Configuring the notification for GCC Fluidics control or GCC Scan control

 In the appropriate instrument control software, click the Email button; or From the Edit menu, select **Email Messages...**

The GCC Email Configuration Editor opens (Figure 434).

Email From To	Address Information		Email Address: Please enter comma separated addresses in the "To" field. Email for fluidics and messages will be sent to the address(s) listed in SMTP Server/Port: This is the name or IP addre	email Save Save Test Em
SMTI Serve	P Server	Pot 25	SMIP server and the port on which the SMIP sent.	email is to be
Scanr	ner Fluidics Da	Subject	Rody A	To enable email for a
	20010	Subject	Erroutile coordina	message, please select
	3201U 20010	Scan error	Connot road or graats on array fils	the email ID column.
	32813	Scanerror	Cannot get the scan parameters fr	The error message
	32814	Scanerror	This array has already been scor	subject can be edited b
	33017	Scan error - Low disk space	Error while scanning. Not enough	corresponding cell.
	33038	Door opened	The door was opened during a sr	When the
	33039	Scanner offline	The scanner network connection	error/information state
Π	33040	Autoloader run started	The user listed in the email starter	occurs, the software will send an email to all use
Π	33041	Autoloader run complete	The autoloader run is complete.	listed in the "To" field in
	33042	Chip loaded	A cartridge was loaded in the auto	Information" group box.
	33043	Scan started	A scan was started in the autoload	The "Powert to Defect"
	33045	Scan aborted	A user aborted a scan in progress	button will revert all the
	33046	Scan complete	The scan was completed.	message settings (subje
	33047	Rescan required	The autoloader door was opened	tab back to the default.
	536900966	Scan error - cannot connect	Cannot connect to the scanner; ch	
_				Revert to Default

- 2. Enter the email account the messages will be sent from in the From box.
- 3. Enter the email account(s) to receive the message in the To... Box
- 4. Enter the SMTP Server and Port information in the appropriate boxes.
- 5. You can click the Test button to send a test e-mail.

6. Select the Scanner or Fluidics tab, depending upon which instrument you want to select messages for (Scanner or Fluidics).

The message list displays the messages you can select from--they correspond to different types of failures or other conditions in the instrument.

Figure 435 Message List for Scanners						
Scan	Scanner Ruidics DataUpload					
	ID	Subject	Body			
	32810	Scan error	Error while scanning.			
	32812	Scan error	Cannot read or create an array file			
	32813	Scan error	Cannot get the scan parameters for			
	32814	Scan error	This array has already been scar			
	33017	Scan error - Low disk space	Error while scanning. Not enough			
	33038	Door opened	The door was opened during a sc			
	33039	Scanner offline	The scanner network connection v			
	33040	Autoloader run started	The user listed in the email started			
	33041	Autoloader run complete	The autoloader run is complete.			
	33042	Chip loaded	A cartridge was loaded in the auto			
	33043	Scan started	A scan was started in the autoload			
	33045	Scan aborted	A user aborted a scan in progress			
	33046	Scan complete	The scan was completed.			
	33047	Rescan required	The autoloader door was opened			
	536900966	Scan error - cannot connect	Cannot connect to the scanner; ch \swarrow			
<			>			

- 7. Select and edit messages:
 - a. Select the check box next to the message ID.
 - b. Click in the subject or body column for the message and edit the text. You can click the Default button to return to the original configuration.
- 8. Click **Save** to save the configuration changes.



Log files generated by GCC

GCC log files

The log files are produced by different GCC components. The logs provide a record of the tasks performed by different components, such as the migration tools and installer.

These log files provide useful information for troubleshooting problems and may be requested by your support person. For details on how to collect and send log files, see "Error logs" on page 41

The following files apply to both Cartridge Systems and GeneTitan Instruments. All the GCC log files from C:\Command_Console\Logs

The different log files include:

Systemlog.XML	XML file with system information.
Workflow.log	Text file with information on workflow status and history.
GCC_LibFileImporter. log (with date and time code)	Text file with info on use of the Library File Importer.

Other GCC Files

Your support person may need the following files for troubleshooting:

- Library files (*.PARAMS, *.MASTER, *.WORKFLOW, *.SMD, *.MEDIA) located in C:\Command_Console\Library, excluding the large analysis library files (CDF, PSI, GRC).
- Provide a list of all sub folders and their contents under the library files folder located in C:\Command_Console\Library. Please ensure there are no duplicate library files, as these can cause problems.
- GCC system configuration file located at C:\Command_Console\Configuration\Calvin.System.config
- 4. Pending job order files located in C:\Command_Console\Jobs
- 5. Other GCC related information, such as:
 - a. The number of files under C:\Command_Console\Data, including sub directory.
 - b. If the system is a networked system or a standalone system.
 - c. Other applications installed on the system, such as antivirus application, MS Office, Internet Explorer versions.



GCC log files for cartridge systems

The following files are instrument-specific log files that apply to GCS 3000/FS 450 Instruments:

fluidics.log	Text file with info on Fluidics Station use
scanner.log	Text file with info on Scan Control use
FS.log (with date and time code)	Text file with information on the Fluidics Script installation.

GCC log files for GeneTitan systems

Log files for the GeneTitan Instrument control processes are placed in subdirectories of the Command Console $Logs \$ folder.

Your support person may need the following files for troubleshooting:

GeneTitan Fluidics

- 1. C:\Command_Console\Logs\96F\
 - a. subdirectories named by date (e.g. Log7-29-2009)
 - Collect all dated directories and contents since the GeneTitan app was started, not just the date of the event (some logging goes into files from the date the app started so this can be critical for us).
 - Absolutely required are all the log directories from the date the run was started to the date of the event.
- 2. C:\Command_Console\Logs\96F\FluidicErrorLog all files in this directory
- 3. C:\Command_Console\RAP2

The main user interface to this logging structure is file is C:\Command_Console\RAP2\RAP.html.

- RAP.html contains historical information (since GCC 4.3 was installed) about what has been run on the system
- RAP.html contains links to locations within the RAP2 folder and to some locations the standard logs found in C:\Command_Console\Logs\96F
- The logging structure supplements the standard logs found in C:\Command_Console\Logs\96F. It does not replace it.
- The RAP2 folder is not on the 30 day log file cleaner path.

GeneTitan MC Imaging Device

- 1. C:\Affymetrix\GeneChipHTScanControlMC\Log collect all dated directories and contents since the GeneTitan app was started
- 2. C:\Affymetrix\GeneChipHTScanControlMC\RunLog collect all dated directories and contents since the GeneTitan app was started.



Collecting GCS3000/FS450 log files

Log files are produced by different GCC components. The logs provide a record of the tasks performed by different components, such as the migration tools and installer.

These log files provide useful information for troubleshooting problems and may be requested by your support person.

1. From the GCC Launcher, click Log Collector.

The Collect Logs window appears. (Figure 436)

Figure 436 Logs Files Collector window	
GeneChip Command Console Log Files Collector	×
applied biosystems	
Days 7 V Collect Logs	

- 2. Click on the **Days** drop-down to select the number of days worth of log files you need to collect.
- 3. Click Collect Logs.

A Collecting logs. Please wait... message appears. (Figure 437)

To terminate a log collection in progress, click **Cancel**.

Figure 437 Logs Files Collector window	
GeneChip Command Console Log Files Collector	×
applied biosystems Days 7 Cancel Collecting logs. Please wait	

After a few moments, a zip file containing your collected logs is placed onto your Desktop for easy access.

TSV files



Using TSV files for batch editing

You can no longer download batch registration or batch editing files in TSV (Tab-Separated-Values) format in GCC, but you can use previously created TSV files. The format of TSV files is discussed here.

The header row in a TSV file includes special properties that define the file and the physical array:

- **Path** The path to where the Sample file is created. Can be used to place Sample files in project folders.
- **Project** The project that the Sample (ARR) file is assigned to.

Note: Specify either the Path or the Project for the files. Specifying both will return an error message.

File Name	Unique identifier for the Sample file.
Array Name	Name assigned to the array during registration.
Probe Array Type	Part number for the array(s).
Barcode	Barcode on the array(s).
Attributes	Additional information about the sample and experiment that you interpret your results.

Path

The path needs to be associated with a data root. You can assign a set of sample files to a particular project if you select that project's folder in the Path field.

Note: Specify either the Path or the Project for the files. Specifying both will return an error message.

Project

Specifying a project for the Sample file will determine the folder the Sample file is created in.

File Name

Enter the name assigned to the Sample file to be created.

can use to

Barcode, array name and array type

If you are using Excel, you can select the probe array type from a drop-down list (Figure 438). The drop-down list can be disabled in Excel if you want to enter multiple arrays for each sample.

Figure 438 List of probe arrays in Excel spreadsheet				
E	=		F	
Probe A	rray Typi	Ba	arcode	Sampl
HG-U13	3A]	-		Batch1
HG-U133	A	^		Batch2
HG-U133	A_2	_		Batch3
HG-0133	5 1330			
Mappings	ISSA SOK Hind24			
Mapping5	OK_Xba24			
Test3	-			
Test3_be	ns	<u>×</u>		

You can also enter multiple array information into the file.

Note: You can use custom barcodes to register an array in Batch Registration.

Entering multiple arrays

- 1. Enter a comma-delimited list in the barcode column: FirstArrayBarcode, SecondArrayBarcode
- 2. Enter a comma-delimited list in the array name column: FirstArrayName, SecondArrayName
- 3. Enter a comma-delimited list in the Array Type column: FirstArrayType, SecondArrayType

Attributes

Enter the values for the attributes in the appropriate columns.

GCC uses two types of attributes for Batch Registration:

- Template Attributes: Attributes that have been defined in a template. When you select templates for the downloaded batch registration file, the array attributes in those templates are included as headings in the batch registration file.
- User Attributes: Attributes that you add in the Batch Register file. You create a user attribute by entering the attribute name and other characteristics in the column header, and then entering attribute values in the appropriate cells.

Attributes need to have the following characteristics defined:

- AttributeName
- TemplateName (if any; not used for User Attributes)
- DataType

Different methods are used for defining attribute characteristics in TSV and Excel format, as described below.

TSV format

In TSV format, all of the attribute characteristics are defined in the column header, as shown in the template below.

- Header format for Template Attribute: AttributeName:TemplateName:DataType
- Header format for User Attribute: AttributeName:*:DataType

Reconnector



Introduction

Use the Reconnector to restore file associations among Drop and Scan data files (DAT, CEL, and CHP) and a pre-registered Sample (ARR) file on the network.

The types of data and files used in GCC, the methods used to track relationships between files, and the types of problems that can occur are described below.

The GCC software tracks:

- Information about the experiment, sample, and array(s)
- Probe array data
- Other information about probe array processing

GCC uses the file types to store array information and data, as shown in Figure 439.





- Information about the sample, experiment, and physical array are collected in Sample (ARR) files.
- Probe array data generated during scanning and processing are collected in Data files of various types.
 - Image Data (DAT)
 - Cell Intensity Data (CEL)
 - Probe Intensity Data (CHP)

Note: Array data files in GCC use the same file extensions as in GCOS, but they are in a different format; GCOS-format array data files cannot be viewed using GCC tools, such as the GCC Viewer. You can use DEC to convert GCOS-format files into GCC format.

The DAT, CEL and CHP data files all have parent-child relationships, as shown in Figure 440.

Figure 440 File Hierarchy displayed in GCC

3 Arrays.		
🖽 🖥 🔲 @511	38800311229011406401149883291B.ARR (Sa
🗄 📔 🔲 @511	38800311229011406401149883294A.ARR (Sa
🖻 📔 🗌 Test_l	File_01.ARR (Sample)	
ė. 🖸 🗋	Test_FIle_01 (Array)	
ė- 🌉 [Test_FIle_01.DAT	
.	Test_FIle_01.CEL	
	Test_FIle_01.CHP	
	—	

In GCC the lineage information for probe array data files is preserved using GUIDs, or Globally Unique Identifiers. A GUID is a number that is unique to that file. Each sample and data file is assigned a GUID for tracking file lineage information (Figure 441).



- Other files containing additional information about the probe array processing
 Info about processing the array (AUDIT)
 - Sub-grid information (GRD) (only for arrays with sub-grids)
 - JPEG image (JPG) (only for arrays with sub-grids?)

Connecting files

Drop and scan data files and preregistered sample files There are also circumstances where you can have multiple (commonly two) sample files for the same array, which is an error condition in GCC. This can happen when you perform scans on arrays with sample (ARR) files on a network data root and a problem arises with the network connection.

You can create Sample (ARR) files on any data root your GCC system has access to, including network data storage. (Figure 442)



However, you cannot create DAT files over a network connection to network data storage; instead, the DAT files are created in the default folder on the Scanner Workstation computer. (Figure 443)

This is done to protect the DAT file from any problems related to the networks, so that an array can always be scanned successfully even when a network is unreliable.



The Upload Data function can be used to automatically transfer DAT and CEL files from the Default folder to the network data storage where the Sample (.ARR) file is located. (Figure 444)

Upload Data is useful when you wish to consolidate data from different workstation computers onto one network data storage site.



If the network connection between the network data root and the scanner workstation fails during the scan, the actual scan isn't affected. However, the links between the Sample file on the network data root and the DAT and CEL files on the Scanner workstation will be broken, and a a new Sample (ARR) file is created in the Scanner Workstation default folder (with the array barcode used as a name). (Figure 445)



In this case, you cannot use the GCC Upload Data function to transfer the array data files to the Network Data Root. You can transfer the Sample and Data files manually, using Windows Explorer or another tool. (Figure 446)



After transferring the Sample and Data files to the network data root, you can use the Connect Drop and Scan Data Files and pre-registered ARR file function of the Reconnect tool to associate the DAT and CEL files with the preregistered Sample File, and to merge the sample file data from the drop and scan files. (Figure 447)

 $\langle \cdot \rangle$



Starting Reconnector

IMPORTANT! All files to be reconnected in a particular operation must be in the same source folder and must be in GCC format before reconnecting.

1. From the GCC Launcher, click **Reconnector**.

The Welcome to the Reconnector window appears. (Figure 448)

Figure 448 Welcome window

appliedbiosystems - Reconnector	-		×
Welcome to the appliedbiosystems Reconnector Please select the type of operation that you wish to perform.			*
The appliedbiosystems Reconnector is designed to enable the user to establish appropriate relationships among files in (This tool can be used to establish appropriate relationships between DEC imported DAT and CEL files, between DEC im and CHP files or between the drop and scan data files (DAT, CEL and CHP) and the pre-registered ARR file as a batch of	Commanc ported CE peration.	l Cons L	sole.
Caution: Please read the appliedbiosystems Reconnector User's Guide carefully before using the application. Select an operation.			
Reconnect DAT and CEL files (batch operation) This paties exceeds the upperturbation operation)			
(This option enables the user to recommercial of the converted command consule DAT and CEL lifes in a given tolder.)			
O Reconnect CEL and CHP files (batch operation) (This option enables the user to reconnect all of the converted Command Console CEL and CHP files in a given folder.)			
Reconnect Drop and Scan data files to pre-registered ARR (batch operation) (This option enables the user to reconnect all of the DAT, CEL and CHP files to a pre-registered ARR file on the network. As a part of reconnection the drop and scan ARR file will be merged with the pre-registered ARR.)			
appliedbiosystems Reconnector			
Version: 5.00.259 ® 2018 Thermo Fisher Scientific Inc. All rights reserved. appliedbiosystems and GeneChip are registered trademarks used by ThermoFisher Scientific.			
Heb	ncel < Ba	ick	Next >

The Reconnect Drop and Scan Data Files and pre-registered ARR (batch operation) option (Figure 449) enables you to:

- Select the folder with the files you wish to merge. Please ensure that the drop and scan ARR and associated data files (DAT, CEL, and CHP) and the preregistered ARR files are in the same source folder.
- Review and change the proposed relationships among the files in the folder.
- Reconnect the Drop and Scan data files with the pre-registered ARR files.

IMPORTANT! As a part of this operation the contents of the drop and scan ARR file will be merged with the pre-registered ARR file and the DAT, CEL, and CHP files will be renamed using the array name from the pre-registered ARR files.

Figure 449	
appliedbiosystems - Reconnector	
Batch Reconnection - Drop and Scan ARR and Pre-register ARR	*
Instruction Before beginning the operation, please ensure that the drop and scan ARR and associated data files (DAT, CEL and CHP) and the pre-registered ARR files are in the same source folder. Step 1: Select the source folder for the files to be reconnected. Step 2: Establish the proper file relationships by using either the Break and/or Join button. Step 3: Click the reconnect button.	
Step 1: Select the folder location of source files to reconnect	
E:\Reconnector Data	Browse
Step 2: Establish the proper file associations by using the Break and Join button	
۲. III	Þ
Remove Selected Break Join Display Options Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Construction of the selected Image: Constructid Image: Constructio	
Help Filter Cancel	< Back Reconnect

Merging data files associated with drop and scan ARR and pre-registered ARR files

1. Make sure that the files you want to merge are all in the same folder, or in a subfolder within the folder

Selecting the folder

- 1. Enter the path in the select folder location box; or
- 2. Click Browse.

The Browse for Folder window opens.

3. Navigate to the location of the folder, click to highlight it, then click **OK**.

The Drop and Scan data files and pre-registered Sample (ARR) files in the folder and its sub-folders are displayed in a file list window. (Figure 450)

Figure 450		
Step 2: Establish the proper file associations by using	g the Break and Join button	
▲ DAT File	CEL File	Status
+ .\051404KW_P05a.DAT		
+	.\051404KW_P05a.CEL	
\@51138800311229011406401149883294A.DAT		
🛨	.\@51138800311229011406401149883294A.CEL	
	- Display Options	
Remove Selected Break Jo	Matched: U V Unmatched: 4	Error: U Varning: U

The file list window has four columns:

Status Icon	+ Unmatched: Indicates unmatched file
	Error: Indicates naming match between incompatible files
	Matched: Indicates match between compatible files.
	Marning: Indicates compatible files with tentative parent-child
	connections, but some information mismatch.
Drop and Scan ARR File	Sample (ARR) file created during Drop and Scan.
Pre-register ARR File	Sample (ARR) file created using sample registration functions of GCC Portal.
Status	Messages if files are not compatible.

IMPORTANT! Even though only the Drop and Scan ARR file is displayed in the window, the reconnect operation will connect all the associated data files (DAT, CEL, and CHP) with the pre-registered ARR file.

Click the check box(es) to select/deselect (show/conceal) these different display options:

- **Matched** Files with tentative parent-child connections.
- **Unmatched** Files with no tentative parent-child connections.
- **Error** Incompatible files with tentative parent-child connections.
- **Warning** Compatible files with tentative parent-child connections but some information mismatch.

Use the bottom buttons to:

- Remove Selected Remove selected/highlighted file(s).
- Break Break current connections between files.
- Join Join files that are not yet connected.
- Click Filter to show a list of files that are not eligible for the merge operation. (Figure 451)

Figure 451 Filter List



Breaking the tentative connection between two files

- 1. Click in the row with the files you want to break.
- 2. Click the Break button.

Note: You can only break connections previously joined files.

Joining two unconnected files

 Select the files you wish to join by holding down the Ctrl key while you click on each file. (Figure 452)

Figure 452		
Step 2: Establish the proper file associations by usin	g the Break and Join button	
▲ Drop and Scan ARR File	Pre-register ARR File	Status
📢 🔇 .\@52006500461817101308401416533701.ARR	\Pre_Register_01.ARR [Pre_Register_01_(HG-U133A_2)]	
.\@52006500461817101308401416533702.ARR	\Pre_Register_02.ARR [Pre_Register_02_(HG-U133A_2)]	
.\@52006500461817101308401416533703.ARR	.\Pre_Register_03.ARR [Pre_Register_03_(HG-U133A_2)]	
.\@51059900413526052906400976113289.ARR		
\@52006500461817101308401416533704.ARR		
🛨	.\Pre_Register_04.ARR [Pre_Register_04_(HG-U133A_2)]	
<		>
	Display Options	
Remove Selected Break Jo	in 🔽 Matched: 3 🔽 Unmatched: 3 🗹 Error:	0 🗹 Warning: 0

2. Click the **Join** button.

Note: If the Join operation is not successful, an error message detailing the discrepancies appears. Acknowledge the message, then click **OK**.

If the Join operation is successful, the new parent-child relationship is displayed in the file list. (Figure 453)

Figure 453	Batch	Reconnection	window
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appliedbiosystems - Reconnector				_ 🗆 X
Batch Reconnection - Drop and Scan ARR	and Pre-register ARR			*
Instruction Before beginning the operation, please ensure the pre-registered ARR files are in the same so Step 1: Select the source folder for the files to Step 2: Establish the proper file relationships b Step 3: Click the reconnect button.	that the drop and scan ARR ource folder. be reconnected. y using either the Break and	and associated data files (DAT, CEL and I/or Join button.	CHP) and	
Step 1: Select the folder location of source files	to reconnect			
E:\Reconnector Data				Browse
Sten 2: Establish the proper file associations b	using the Break and Join h	wittop		
Drop and Scan APP File	Pre-register ADD File	Statue		
•				- F
Remove Selected Break	Join	Display Options Image: Matched: Image: Matched:	Error: 0 🗹 Warning: 0	
Help Filter			Cancel	< Back Reconnect

3. After joining is complete, click **Reconnect** to connect all matched files. The Reconnect Status window appears. (Figure 454)

Batch Merge Status

The Reconnect Status window displays the status of the different attempts at merging Sample (ARR) files.

Figure 454 Reconnect Status window

appliedbiosystems - Reconnector	· · · · · ·		
Reconnect Status 100% Update CEL fie [E:\Reconnector Data\@510599	00121212121212121212120007.CEL]		*
Drop and Scan ARR File	Pre-register ARR File	Status	
.\@5105990012121212121212121212120007.ARI	R .\sample007.ARR [sample007_(Te	st3)] Update CEL file [E:\Rec	onnector l
•			Þ
Help		Cancel < Back	Stop

The list displays the files that have had their connections changed, with the following information:

Status Icon	Unmatched: Indicates unmatched file	
	S Error: Indicates naming match between incompatible files	
	Matched: Indicates match between compatible files.	
	A Warning: indicates compatible files with tentative parent-child connections, but	
	some information mismatch.	
Parent File	Parent file.	
Child File	Child file.	
Status	Status of connect operation.	

Click **Log** (bottom left) to open a file giving log information about the reconnect operations.

For support visit **thermofisher.com/support** or email **techsupport@lifetech.com** thermofisher.com

